

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 102.427 Seconds
(without alignments)
508.875 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 LBSGQVLVXPSTGLSLTCTV.....RSDGYTLDMWGQGLVTVSS 114

Scoring table: BLOSUM62
Gapop :0.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	5	ABG30446 Human IGE
2	608	99.0	114	5	ABG30447 Human IGE
3	546	88.9	114	5	ABG30445 Human IGE
4	518.5	84.4	121	10	Aef71064 High fireq
5	514.5	83.8	140	9	Adx98269 Human ant
6	511	83.2	128	8	ADP22124 Human ant
7	511	83.2	128	8	ADP22104 Human ant
8	511	83.2	128	8	ADP22096 Human ant
9	510.5	83.1	121	7	ADP03982 Murine-ex
10	510	83.1	118	7	ADP03968 Murine-ex
11	509.5	83.0	123	7	ADP03870 Murine-ex
12	507.5	82.7	125	7	ADP03871 Murine-ex
13	507	82.6	120	7	ADP03974 Murine-ex
14	507	82.6	120	7	ADP03873 Murine-ex
15	507	82.6	122	7	ADP03977 Murine-ex
16	507	82.6	473	4	AAB36206 Human imm
17	506.5	82.5	119	9	ADX98416 Human ant
18	506	82.4	221	7	ADJ32126 Human int
19	505.5	82.3	121	7	ADP03981 Murine-ex
20	505	82.2	128	8	ADP22120 Human ant
21	504.5	82.2	117	7	ADG9784 Anti-huma
22	504.5	82.2	117	7	ADDO5388 Anti-MUC1
23	504.5	82.2	117	7	Adf09826 Human ant

ALIGNMENTS

24	503.5	82.0	119	7	ADP03970	Adp03970 Murine-ex
25	503.5	82.0	148	10	AEE94855	Aee94855 Antibody
26	503.5	82.0	148	10	AEE94833	Aee94833 Antibody
27	502.5	81.8	123	2	AAW78433	Aaw78433 Antibody
28	502.5	81.8	123	5	ABB7976	Abb7976 Heavy cha
29	502.5	81.8	123	7	ADG88414	Adg88414 anti-OB-R
30	502.5	81.8	123	7	ADP03872	Adp03872 Murine-ex
31	502.5	81.8	144	9	ADX98263	Adx98263 Human ant
32	502	81.8	122	9	AEA21492	Aea21492 Human ant
33	502	81.8	124	7	ADP03935	Adp03935 Murine-ex
34	501	81.6	125	8	AD516556	Ad516556 Human ant
35	501	81.6	130	9	AEBO1018	Aeb01018 Human IPI
36	501	81.6	252	5	ABP45318	Abp45318 Human Bly
37	501	81.6	252	7	ADG96145	Adg96145 Single ch
38	501	81.6	252	9	AED78198	Aed78198 Human B I
39	500.5	81.5	127	4	AAG80217	Aag80217 Human aut
40	500	81.4	120	7	ADP03958	Adp03958 Murine-ex
41	500	81.4	120	7	ADP03969	Adp03969 Murine-ex
42	500	81.4	121	7	ADJ80377	Adj80377 Antibody
43	500	81.4	121	8	AD516559	Ad516559 Human ant
44	500	81.4	126	3	AAB30584	Ab30584 A human v
45	500	81.4	126	5	ABP54970	Abp54970 Anti-Idio

RESULT 1	ABG30446	standard; protein; 114 AA.
ID	ABG30446;	
XX	ABG30446;	
AC	21-OCT-2002	(first entry)
XX		
DE	Human IGE Fab clone 60 heavy chain protein.	
XX		
KM	Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;	
KW	timochy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..26
FT	Region	/note="FR1 region"
FT	Region	27..33
FT	Region	/note="CDR1 region"
FT	Region	34..47
FT	Region	/note="FR2 region"
FT	Region	48..63
FT	Region	/note="CDR2 protein"
FT	Region	64..95
FT	Region	/note="FR3 region"
FT	Region	96..103
FT	Region	/note="CDR2 region"
FT	Region	104..114
FT	Region	/note="FR4 region"
PN	WO200253595-A1.	
PD	11-JUL-2002.	
XX		
PF	27-DEC-2001, 2001WO-SR002908.	
XX		
PR	29-DEC-2000, 2000SE-00004892.	
XX		
PA	(PHAA) PHARMACIA DIAGNOSTICS AB.	
XX		
PI	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX	WPI, 2002-583604/62.	
DR	N-PsDB; ABR9638.	
XX		

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or Igg comprising
 PT variable region of group 2 allergen specific-human Igg Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 37; 45pp; English.

CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human Igg Fabs and methods for their use. The proteins
 CC of the invention may have anti-allergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's Igg
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific Fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The Fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific Fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC Igg antibodies to Phi p 2. The present sequence represents the human Igg
 CC Fab, clone 60 heavy chain protein of the invention

CC Sequence 114 AA;

Query Match 100.0%; Score 614; DB 5; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1,2e-44;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LBSGPGIVKPSQTLSTCTVSGSIRSGYVSWVROPKGLGEMIGNIYHSGNTYVPS 60
 Db 1 LBSGPGIVKPSQTLSTCTVSGSIRSGYVSWVROPKGLGEMIGNIYHSGNTYVPS 60

QY 61 LKSRITMSVDTSKNHSRLRTSTVAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
 Db 61 LKSRITMSVDTSKNHSRLRTSTVAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 2

ABG30447 ID ABG30447 standard; protein; 114 AA.

AC ABG30447;

XX 21-OCT-2002 (first entry)

XX Human Igg Fab clone 100 heavy chain protein.

XX Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
 KM timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..26 /note= "FR1 region"

FT Region 27..33 /note= "CDR1 region"

FT Region 34..47 /note= "FR2 region"

FT Region 48..63 /note= "CDR2 protein"

FT Region 64..95 /note= "FR3 region"

FT Region 96..103 /note= "CDR2 region"

FT Region 104..114 /note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

PF 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

DR MPI; 2002-583604/62.

XX N-PSDB; ABK89639.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or Igg comprising
 PT variable region of group 2 allergen specific-human Igg Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 38; 45pp; English.

CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human Igg Fabs and methods for their use. The proteins
 CC of the invention may have anti-allergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's Igg
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific Fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The Fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific Fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC Igg antibodies to Phi p 2. The present sequence represents the human Igg
 CC Fab, clone 100 heavy chain protein of the invention

CC Sequence 114 AA;

Query Match 99.0%; Score 608; DB 5; Length 114;
 Best Local Similarity 97.4%; Pred. No. 3.9e-44;
 Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LBSGPGIVKPSQTLSTCTVSGSIRSGYVSWVROPKGLGEMIGNIYHSGNTYVPS 60
 Db 1 LBSGPGIVKPSQTLSTCTVSGSIRSGYVSWVROPKGLGEMIGNIYHSGNTYVPS 60

QY 61 LKSRITMSVDTSKNHSRLRTSTVAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
 Db 61 LKSRITMSVDTSKNHSRLRTSTVAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 3

ABG30445 ID ABG30445 standard; protein; 114 AA.

AC ABG30445;

XX 21-OCT-2002 (first entry)

XX Human Igg Fab clone 94 heavy chain protein.

XX Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
 KM timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..26 /note= "FR1 region"

FT Region 27..33 /note= "CDR1 region"

FT Region 34..47 /note= "FR2 region"

FT Region 48..63 /note= "CDR2 protein"

ADX98269
 ID ADX98269 standard; protein; 140 AA.
 AC ADX98269;
 DT 05-MAY-2005 (first entry)
 XX
 DE Human anti-HGF antibody heavy chain variable region protein - SEQ 41.
 XX
 KM antibody; cytostatic; cancer; neoplasm; solid tumor;
 KM hepatocyte growth factor; HGF; light chain variable region.
 XX
 OS Homo sapiens.
 XX
 PN WO2005017107-A2.
 XX
 PD 24-FEB-2005.
 XX
 PD 16-JUL-2004; 2004WO-US018936.
 PF 16-JUL-2003; 2003US-0488681P.
 PR 18-JUL-2003; 2003US-0488681P.
 XX
 PA (AMGE-) AMGEN INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Burgess TL, Coxon A, Green LL, Zhang K;
 DR WPI; 2005-182350/19.
 XX
 DR N-PSDB; ADX98246.
 XX
 PT New polypeptide comprising a complementarity determining region (CDR)
 PT consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
 PT binding hepatocyte growth factor, useful in preparing a composition for
 PT treating cancer.
 XX
 PS Claim 9; SEQ ID NO 41; 301pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide comprising at least
 CC one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
 CC or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
 CC an antibody heavy or light chain, is capable of binding hepatocyte growth
 CC factor (HGF). HGF, also known as scatter factor (SF), has been identified
 CC as a potent mitogen for hepatocytes and also as a secretory protein of
 CC fibroblasts and smooth muscles that acts to induce motility of epithelial
 CC cells. The polypeptide demonstrates cytostatic activity and may be useful
 CC in preparing a composition for treating cancer or a solid tumor. The
 CC current sequence is that of the human anti-HGF antibody heavy chain
 CC variable region protein - SEQ 41 of the invention.
 XX
 SQ Sequence 140 AA;
 Query March 83.8%; Score 514.5; DB 9; Length 140;
 Best Local Similarity 84.5%; Pred. No. 4.4e-36;
 Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
 QY 2 ESGGGLVPSQTLTLCTVSGSGSIRSGYVSWVROPKGLKLEWIGNIYHSGNTYVPSL 61
 Db 25 ESGGGLVPSQTLTLCTVSGSGSIRSGYVSWVROPKGLKLEWIGNIYHSGNTYVPSL 84
 QY 62 KSRITMSVDTSKNHPSLRLISVTADTAIVYVCARS---DGYTLDNWGCGTLVTVSS 114
 Db 85 KSRVTMSVDTSKNHPSLRLISVTADTAIVYVCARDPLVGDYGFDPWCGTLVTVSS 140
 RESULT 6
 ADP22124
 ID ADP22124 standard; protein; 128 AA.
 AC ADP22124;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:30.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KM antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KM neuroprotective; vasotropic; immunosuppressive; nephrotropic;
 KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KM prostate cancer; immuno-mediated inflammatory disease;
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KM restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KM septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050683-A2.
 XX
 PD 17-JUN-2004.
 XX
 PD 02-DEC-2003; 2003WO-US038281.
 PF 02-DEC-2002; 2002US-0430729P.
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 PA (ABGE-) ABGENIX INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 XX
 DR WPI; 2004-480601/45.
 DR N-PSDB; ADP22123.
 XX
 PT New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 30; 213pp; English.
 XX
 CC The present invention describes a human monoclonal antibody (1) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with
 CC (1), and detecting the level of binding between the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (1) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 128 AA;

Query Match 83.2%; Score 511; DB 8; Length 128;
 Best Local Similarity 78.9%; Pred. No. 7.9e-36;
 Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGYVSWVROPCKGLMIGNIYHSGTYNPSL 61
 DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGYVSWVROPCKGLMIGNIYHSGTYNPSL 65
 QY 62 KSRITMSVDTSKNPFSLRLTSTVTAADTAVYYCARSDG-----YTLDMNGGCTLV 111
 DB 66 KSRVITSVDTSKNPFSLRLTSTVTAADTAVYYCARSDGNYNMNDVYDGLDVGQGTIVT 125
 QY 112 VSS 114
 DB 126 VSS 128

RESULT 7
 ADP22104
 ID ADP22104 standard; protein; 128 AA.
 XX ADP22104;
 AC
 XX 09-SEP-2004 (first entry)
 DT
 XX
 XX Human anti-TNFa antibody heavy chain variable region SEQ ID NO:10.
 DE
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipneumonia; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 XX Homo sapiens.
 OS
 XX MO2004050683-A2.
 PN
 XX 17-JUN-2004.
 PD
 XX 02-DEC-2003; 2003MO-US038281.
 PF
 XX 02-DEC-2002; 2002US-0430729P.
 PR
 XX
 XX (ABGE-) ABGENIX INC.
 PA
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendescho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenchu K, Faggioni R, Senaldi G, Qiaojuan JS;
 PI WPI; 2004-480601/45.
 DR N-PSDB; ADP22103.
 DR
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 XX Example 10; SEQ ID NO 10; 213pp; English.
 PS
 XX The present invention describes a human monoclonal antibody (i) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with

CC (1), and detecting the level of binding between the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipneumonia, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (1) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFa
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.

XX
 XX Sequence 128 AA;
 SQ

Query Match 83.2%; Score 511; DB 8; Length 128;
 Best Local Similarity 78.9%; Pred. No. 7.9e-36;
 Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGYVSWVROPCKGLMIGNIYHSGTYNPSL 61
 DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGYVSWVROPCKGLMIGNIYHSGTYNPSL 65
 QY 62 KSRITMSVDTSKNPFSLRLTSTVTAADTAVYYCARSDG-----YTLDMNGGCTLV 111
 DB 66 KSRVITSVDTSKNPFSLRLTSTVTAADTAVYYCARSDGNYNMNDVYDGLDVGQGTIVT 125
 QY 112 VSS 114
 DB 126 VSS 128

RESULT 8
 ADP22096
 ID ADP22096 standard; protein; 128 AA.
 XX ADP22096;
 AC
 XX 09-SEP-2004 (first entry)
 DT
 XX
 XX Human anti-TNFa antibody heavy chain variable region SEQ ID NO:2.
 DE
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipneumonia; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 XX Homo sapiens.
 OS
 XX MO2004050683-A2.
 PN
 XX 17-JUN-2004.
 PD
 XX 02-DEC-2003; 2003MO-US038281.
 PF

```

XX 02-DEC-2002; 2002US-0430729P.
PR (ABGE-) ABGENIX INC.
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
XX Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX WPI; 2004-480601/45.
DR N-PSDB; ADP22095.
XX
XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
XX Example 10; SEQ ID NO 2; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (I) that
XX specifically binds to tumor necrosis factor-alpha (TNFa) and comprises:
XX (a) a heavy chain complementarily determining region 1 (CDR1) having the
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX (M1) the level of TNFa in a patient sample, comprising contacting with
XX (1), and detecting the level of binding between the antibody and TNFa in
XX the sample; (2) a composition comprising the antibody or its functional
XX fragment and a carrier; (3) treating (M2) an animal suffering from a
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an
XX animal in need of treatment for the disease by administering the human
XX monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
XX apoptosis in an animal by selecting an animal in need of treatment for
XX TNFa induced apoptosis by administering the human monoclonal antibody of
XX (I). (I) has anabolic, antiarteriosclerotic, antithrombotic,
XX antibacterial, antiinflammatory, antiproliferic, antihematic, eating-
XX disorders, immunomodulator, immunosuppressive, nephrotoxic,
XX neuroprotective, vasotropic and antiapoptotic activities, and can be used
XX as a TNFa antagonist. The antibody (I) is useful in the preparation of
XX a medicament for treating TNF induced apoptosis, neoplastic disease such as
XX breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
XX stomach cancer, endometrial cancer, kidney cancer, colon cancer,
XX pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
XX diseases such as rheumatoid arthritis, glomerulonephritis,
XX atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
XX disease, graft-host reactions, septic shock, cachexia, anorexia, and
XX multiple sclerosis. The present sequence represents a human anti-TNFa
XX antibody heavy chain variable region, which is used in the
XX exemplification of the present invention.
XX
XX Sequence 128 AA:
SQ
Query Match 83.2%; Score 511; DB 8; Length 128;
Best Local Similarity 78.9%; Pred. No. 7.9e-36;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
QY 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPPGKGLWIGNTYHSGNTYVNSL 61
DB 6 ESGGGLVPSQTLSTCTVSGSGSISGGYVSWIRQHPGKGLWIGNTYHSGNTYVNSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYVCARSDG-----YTLDMNGCGTLVLT 111
DB 66 KSRVTISVDTSKNHFSLRLTSVTAADTAAYVYVCARSDGNGYNNDEVYDGLDVGQGTIVT 125
QY 112 VSS 114
DB 126 VSS 128

```

```

AC ADP03982;
XX 29-JUL-2004 (first entry)
XX
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
DE
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytostatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002MO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J, Foltz I, Handa M, Gallo M;
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 152; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 121 AA:
SQ
Query Match 83.1%; Score 510.5; DB 7; Length 121;
Best Local Similarity 82.8%; Pred. No. 8.2e-36;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
QY 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYVSWRQPPGKGLWIGNTYHSGNTYVNSL 61
DB 6 ESGGGLVPSQTLSTCTVSGSGSISGGYVSWIRQHPGKGLWIGNTYHSGNTYVNSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYVCARSDG-----GYTDMNGCGTLVWSS 114
DB 66 KSRVTISVDTSKNHFSLRLTSVTAADTAAYVYCAVYDILTGYAPDIMGQGTWTVSS 121

```

```

RESULT 9
ADP03982
ID ADP03982 standard; protein; 121 AA.
XX

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```

RESULT 10
ADP03968
ID ADP03968 standard; protein; 118 AA.
XX
XX ADP03968;
XX
XX 29-JUL-2004 (first entry)
XX
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX

```

XX	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cervical; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
OS	Unidentified.
XX	
PN	WO2003048328-A2.
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) AGENIX INC.
PI	Gudas J, Foltz I, Handa M, Gallo M;
DR	WPI; 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Example 2; SEQ ID NO 138; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mAb)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated via the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	
SO	Sequence 118 AA;
XX	
Query Match	83.1%; Score 510; DB 7; Length 118;
Best Local Similarity	85.0%; Pred. No. 8.8e-36;
Matches	96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY	
2	ESGGRVNESQTLSTCTVSGSGSIRSGYMSWVRQPRKGLRWGNITVHSGNTVYNSL 61
DB	6 ESGRPLVPSQTLSTCTVSGSGSISGGYMSWVRQHGKGLRWGITYVSGSTVYNSL 65
QY	62 KSRITMSVDTSKNHPSRLRTSVTAADTVAVVYCARSDGVTLDNMGGTLVTVSS 114
DB	66 KSRVTVISDTSKNGPSLSTSSVTADTVAVVYCARVYSGSGSDVWGCTLVTVSS 118
RESULT 11	
ADP03870	
ID	ADP03870 standard; protein; 123 AA.
XX	
AC	ADP03870;
XX	
DT	29-JUN-2004 (first entry)
XX	
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
XX	
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	

OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) AGENIX INC.
PI	Gudas J, Foltz I, Handa M, Gallo M;
XX	
DR	WPI; 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PP	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Claim 1; SEQ ID NO 10; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cyrostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated by the introduction of the human CA IX protein into a
XX	transgenic mouse strain.
SQ	
	Sequence 123 AA:
Query Match	83.0%; Score 509.5; DB 7; Length 123;
Best Local Similarity	82.2%; Pred. No. 1e-35;
Matches 97; Conservative	8; Mismatches 8; Indels 5; Gaps 1,
OY	2 ESGGGLVKKPSQTLSLTCTVSGGSIRSGCYTWSWRORPGKLEWIGNIYHSGNTYYNSL 61
DB	6 ESGGGLVKKPSQTLSLTCTVSGGSISGGYYSWMRHPKGKLEWIGIYYSGSTYYNSL 65
OY	62 KSRITMSVDTSIKNFESRLTGTVTADTAIVVYCARS-----DGYTLDMNGOGTLTVSS 114
DB	66 KSRITVISVDTSIKNPFSLKLSSVTADTAIVVYCAAGAKTYGSGSYLDIWGOTLVVSS 123
RESULT 12	
ID	ADP03871
XX	ADP03871 standard; protein; 125 AA.
AC	ADP03871;
XX	
DT	29-JUN-2004 (first entry)
XX	
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KX	gene therapy; murine; mouse; human; heavy chain variable domain.
OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.

PF 02-DEC-2002; 2002WO-US038550.
 XX
 PR 03-DEC-2001; 2001US-0337275P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudäs J, Foltz I, Handa M, Gallo M;
 XX WPI; 2003-523295/49.
 DR
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 PS Claim 1; SEQ ID NO 11; 89pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytosstatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 XX Sequence 125 AA;
 SQ

Query Match 82.7%; Score 507.5; DB 7; Length 125;
 Best Local Similarity 81.7%; Pred. No.1.5e-35;
 Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
 QY 2 ESGPGLVPSQTLSTLCTVSGGSIRSGGYWVWROPKGLKLEWIGNIYHSGNTYNPSTL 61
 DB 6 ESGPGLVPSQTLSTLCTVSGGSIRSGGYWVWIRQHPKGLKLEWIGIYISGNTYNPSTL 65
 QY 62 KSRIYISVDTSKNHFSLRLTSVTAADTAAYYCARSGYT---LDNMGGGTLVTVSS 114
 DB 66 KSRIYISVDTSKNHFSLRLTSVTAADTAAYYCARSGYT---LDNMGGGTLVTVSS 125

RESULT 13
 ADP03974
 ID ADP03974 standard; protein; 120 AA.
 XX
 AC ADP03974;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
 XX
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 XX
 PN WO2003048328-A2.
 PD 12-JUN-2003.
 PF 02-DEC-2002; 2002WO-US038550.
 PR 03-DEC-2001; 2001US-0337275P.
 PA (ABGE-) ABGENIX INC.
 XX

PI Gudäs J, Foltz I, Handa M, Gallo M;
 XX WPI; 2003-523295/49.
 DR
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 PS Example 2; SEQ ID NO 144; 89pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytosstatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 XX Sequence 120 AA;
 SQ

Query Match 82.6%; Score 507; DB 7; Length 120;
 Best Local Similarity 83.6%; Pred. No.1.6e-35;
 Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
 QY 2 ESGPGLVPSQTLSTLCTVSGGSIRSGGYWVWROPKGLKLEWIGNIYHSGNTYNPSTL 61
 DB 6 ESGPGLVPSQTLSTLCTVSGGSIRSGGYWVWIRQHPKGLKLEWIGIYISGNTYNPSTL 65
 QY 62 KSRIYISVDTSKNHFSLRLTSVTAADTAAYYCARSGYT---LDNMGGGTLVTVSS 114
 DB 66 KSRIYISVDTSKNHFSLRLTSVTAADTAAYYCARSGYT---LDNMGGGTLVTVSS 120

RESULT 14
 ADP03873
 ID ADP03873 standard; protein; 120 AA.
 XX
 AC ADP03873;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
 XX
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 XX
 PN WO2003048328-A2.
 PD 12-JUN-2003.
 PF 02-DEC-2002; 2002WO-US038550.
 PR 03-DEC-2001; 2001US-0337275P.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudäs J, Foltz I, Handa M, Gallo M;
 XX WPI; 2003-523295/49.
 DR
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 13; 89pp; English.
XX

CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumor,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, esophageal
CC tumor or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 120 AA;

Query Match 82.6%; Score 507; DB 7; Length 120;

Best Local Similarity 83.6%; Pred. No. 1.6e-35; Mismatches 7; Indels 4; Gaps 2;

Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYHSGNTYYPSTL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYHSGNTYYPSTL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDGRT--LDNMGQGLTVTVSS 114
DB 66 KSRVITISVDTSKNHFSLRLTSVTADTAVYYCAR--DGYNWYFDLWGRGLTVTVSS 120

RESULT 15

ADP03977
ID ADP03977 standard; protein; 122 AA.

XX
AC ADP03977;
XX

DT 29-JUN-2004. (first entry)

XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.

XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumor antigen;
KW cytostatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; esophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX
OS Unidentified.

XX
PN WO2003048328-A2.

XX
PD 12-JUN-2003.

XX
PF 02-DEC-2002; 2002WO-US038550.

XX
PK 03-DEC-2001; 2001US-0337275P.

XX
PA (ABGE-) ABGENIX INC.

XX
PI Gudae J, Poltz I, Handa M, Gallo M;

XX
DR WPI; 2003-523295/49.

XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX
PS Example 2; SEQ ID NO 147; 89pp; English.

XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumor,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, esophageal
CC tumor or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 122 AA;

Query Match 82.6%; Score 507; DB 7; Length 122;

Best Local Similarity 82.1%; Pred. No. 1.6e-35; Mismatches 9; Indels 4; Gaps 1;

Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYHSGNTYYPSTL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYHSGNTYYPSTL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYYCAR--SDGYTLDNMGQGLTVTVSS 114
DB 66 KSRVITISVDTSKNHFSLRLTSVTADTAVYYCARYYDILTGMDWVGQGLTVTVSS 122

Search completed: August 30, 2006, 00:41:49
Job time : 103.427 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 10.7091 Seconds
(without alignments)
1024.243 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 ESQGPGLVKSQTLSTLCTV.....RSDGYTLDMWGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR #0:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.5	81.4	135	2 S78051	Ig heavy chain pre
2	495.5	80.7	147	2 S13519	Ig heavy chain V r
3	487	79.3	130	2 S30534	Ig heavy chain V r
4	480.5	78.3	121	2 S44113	Ig heavy chain V r
5	478.5	77.9	140	2 I37782	Ig variable region
6	477.5	77.8	146	2 S09710	Ig heavy chain V r
7	474.5	77.3	116	2 S37456	Ig mu chain - huma
8	474.5	77.3	130	2 S31690	Ig heavy chain V r
9	474	77.2	122	2 S69912	Ig V-D-J region (N
10	473.5	77.1	128	2 S31514	Ig heavy chain - h
11	472.5	77.0	127	2 S19668	Ig heavy chain V r
12	469	76.4	137	2 S31676	Ig heavy chain V r
13	468.5	76.3	123	2 S30530	Ig heavy chain V r
14	465.5	75.8	155	2 S31511	Ig heavy chain - h
15	463.5	75.5	155	2 S31512	Ig heavy chain - h
16	462	75.2	139	2 S31586	Ig heavy chain V r
17	460.5	75.0	146	2 S09711	Ig heavy chain V r
18	460	74.9	145	2 S78055	Ig heavy chain pre
19	459.5	74.8	109	2 PH1673	Ig heavy chain V r
20	457	74.4	110	2 S44110	Ig heavy chain V-D
21	455	74.1	99	2 S26803	Ig heavy chain V r
22	454	73.9	139	2 A41287	Ig heavy chain pre
23	453	73.8	99	2 S26801	Ig heavy chain V r
24	452	73.6	129	2 S44114	Ig heavy chain V r
25	450	73.3	99	2 S26802	Ig heavy chain V r
26	450	73.3	135	2 S31604	Ig heavy chain V r
27	447	72.8	118	2 S20780	Ig heavy chain V r
28	446	72.6	99	2 S12418	Ig heavy chain V r
29	444.5	72.4	139	2 S31696	Ig heavy chain V r

30	443	72.1	118	2 A26340	Ig heavy chain pre
31	442.5	72.1	140	2 A49045	Ig heavy chain V r
32	441.5	71.9	132	2 A38911	Ig heavy chain V r
33	441	71.8	99	2 S26800	Ig heavy chain V r
34	441	71.8	126	2 S47010	Ig heavy chain V4.
35	440.5	71.7	129	2 D2H0WA	Ig heavy chain V-I
36	440	71.7	97	2 PL0118	Ig heavy chain V-I
37	440	71.7	99	2 S26899	Ig heavy chain V r
38	439.5	71.6	98	2 S12421	Ig heavy chain V r
39	439.5	71.6	140	2 A24770	hypothetical hybr
40	439	71.5	140	2 S78052	Ig heavy chain pre
41	438.5	71.4	123	2 S30529	Ig heavy chain V r
42	438	71.3	120	2 PT0370	Ig mu chain precu
43	437	71.2	124	2 S31684	Ig heavy chain V r
44	435.5	70.9	134	2 S54906	Ig heavy chain V r
45	434.5	70.8	98	2 S26902	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S78051
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78051, S23716
R:Hardinath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78051
A:Molecule type: mRNA
A:Residues: 1-135 <HAR>
A:Cross-references: UNIPARC:UPI000015587; EMBL:X54437; NID:937814; PIDN:CA38306.1; PID
R:Hardinath, N.; Goldfarb, I.S.; Ikematsu, H.; Butters, S.E.; Wilder, R.L.; Nockins,
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hu
patient.
A:Reference number: S23716; MID:92031262; PMID:1718404
A:Accession: S23716
A:Molecule type: mRNA
A:Residues: 13-111 <HAW>
A:Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F:14-13/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:27-111/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 499.5; DB 2; Length 135;
Best Local Similarity 79.7%; Pred. No. 1.1e-37;
Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESQGPGLVKSQTLSTLCTVSGSIRSGYVSWVRPQKGLKLEWIGNIYHSGNTYVPSL 61
Db 18 ESQGPGLVKSQTLSTLCTVSGSIRSGYVSWVRPQKGLKLEWIGNIYHSGNTYVPSL 77

Qy 62 KSRITMSVDTSKKHFSRLSTVTAADTAVYYCAR--SDGYTLDN---WGQGLTVTVSS 114
Db 78 KSRITMSVDTSKKHFSRLSTVTAADTAVYYCARLPGDPTLDGMVWGQGLTVTVSS 135

RESULT 2
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MID:91187691; PMID:2011536
A:Accession: S13519

C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin

Df

Oy

ESGPGLVKPSQTLSTCTVSSGGSIRSGGYWMSWRQPPEKGLEMTGNIVHSGNTYINPSL 61
||||| : ||||| : | ||||| : :: |||||
Eg

ESGPGLVKPSETLSTLCVSVGGSVGGIYMGWTRQPPKGLEWTGISIFISGSTTYNPSSL 84
||||| : ||||| : | ||||| : :: |||||


```

Qy      62 KSRITMSVDJTSKNHPSRLRTSVTAADTAVYVCARSDG-----TLDNWGQGITVLT 111
      ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      85 KSRVTISVDJTLKNNFSJLKLSSTTAADTAVYCTR-PEYGDTSVRKRVNMMDLWGQGITV 143

```

QY	112	VSS	114
Db	144	VSS	146

```

RESULT 7
S37456
I: m chain - human (fragment)
C: Species: Homo sapiens (man)
C: Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C: Accession: S37456
R: McIntosh, R.S.; Tandon, N.; Wetman, A.P.
submitted to the EMBL data library, September 1993
A: Description: Cloning and analysis of human IgM anti- $\gamma$ -H2globulin autoantibodies from
A: Reference number: S37453
A: Accession: S37456
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-116 <MCI>
A: Cross-references: UNIPARC:UPI00001161C0, EMBL:X75024, NID:g40431, PIDN:CMS2932.1, P
C: Superfamily: immunoglobulin V region, immunoglobulin homology
C: Keywords: immunoglobulin
C: 1-6-90/Domain: immunoglobulin homology <IMM>

```

Query Match	77.3%	Score 474.5	DB 2	Length 116
Best Local Similarity	77.8%	Pred. No. 1.5e-35		
Matches 91	Conservative 10	Mismatches 7	Indels 9	Gaps 2

Oy 6 GLVKSQTLISLCTVSGGSIIRSGGYMWSVRPPGKGLMIIGNIYHSGNTYYNPISLSRI 65
| | | | | : | | | | | : | | | | | :
Db 1 GLVKBSQTLISLCTVSGGSSISSGGYMWIRQHKGLEMIIGIYYSGSTYYNPSLSKRV 60

```

QY      66 TMSVDTSKNHSRLTSTAAADTAIVVYCARSDGYT-----LDNWGGTLVTWSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TISVDTSKNFSKLSSVTAADTAIVVYCARG-GYSYGYIYYIMDWNKGITVWSS 116

```

```

RESULT 8
S31690
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R:Accession: S31690
R:CisInlier: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31690
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <CUI>
A:Cross-references: UNIPARC:UPI0000116471, EMBL:Z14199, NID:G30984, PIDN:CAA78568.1, PIR:
C:Superfamily: Immunoglobulin V region, Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
/20-102/Domain: immunoglobulin homology <IMM>

```

Query Match	77.3%	Score 474.5;	DB 2;	Length 130;
Best Local Similarity	76.2%	Pred. No. 1.7e-35;		
Matches 93; Conservative	7;	Mismatches 11;	Indels 11;	Gaps 2;

```

Oy      2  ESGPGLVKPISCTLSLTCTVSGGSIRSGGYWMSWRQPPGKGLEWIGNIYHSGNTYNPSSL 61
          |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
Db      11  ESGPGLVKPISCTLSLTCTVSGGSIS--YMSMSRQPPGKGLEWIGYIYISGNTYNPSSL 68

```

Qy	62	KSRTMSVDSKNHPSLRITSVTAADTAVVYCARSDG-----YTLDMNGQGLTV	112
	:	:	
Db	69	KSRTVTSVDSKNQPSLKTSSVTAADTAVVYCARSSVLWEGELVYFDYNGQGLTV	128

QY 113 SS 114

Db 129 SS 130

RESULT 9
S69912

Ig V-D-J region (ND) - human
C.Species: Homo sapiens (man)
C.Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C.Accession: S69912
R.Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A.Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multiple myeloma
A.Reference number: S69909; MUID:94535315; PMID:8057663
A.Accession: S69912
A.Status: preliminary; nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-122 <SAH>
A.Cross-references: UNIPARC:UPI0000116640; EMBL:E233398; NID:G871347; PIDN:CMA83849.1; PIR:J01422
A.Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are identical to those of the immunoglobulin heavy chain variable region of the IgM antibody
A.Superfamily: immunoglobulin V region, immunoglobulin homology
F15-99/D domain: immunoglobulin homology <IMM>

Query Match	77.2%	Score 474	DB 2	length 123
Best Local Similarity	76.9%	Pred. No.	1.8e-35	
Matches 90	Conservative 11	Mismatches 12	Indels 4	Gaps 1

Qy 2 ESGPELVKPSQTLSTCTVSGSIRSCGYWMSWVRQPPKGLKLEIGNIYHSGNTYYNPSL 61

Db 6 ESGPELVKPSQTLSTCTVSGSIRSCGYWMSWVRQPPKGLKLEIGNIYHSGNTYYNPSL 65

```
OY      62 KSRI TMSVDT SKNHFS LRLTSVTAA DTA VVCARS --- DG YTL DNNGO GTL VTWSS   114
          ||| ::||| | | | | | | | | : | | | | | | | | | | | | | | | | | | |
Db      66 KSRISIVDTSKNQPSLRLKSVTAA DTA VVCARGPFRGTYGLDTNCGOTLVPLSS   122
```

RESULT 10
S31514
I9 heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31514
R:Chastagner, P.; Demaison, C.; Therez, J.; Zouali, M.
submitted to the EMBL Data library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies in Sjögren's syndrome
A:Reference number: S31509
A:Accession: S31514
A:status: preliminary
A:molecule type: mRNA
A:residues: 1-128 <CHA>
A:Cross-references: UNIPARC:UPI00001160FB; EMBL:X69862; NID:G33086; PIDN:CAA49496.1; PID:
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
I22-106/Domain: immunoglobulin homology <IMM>

Query Match	77.1%	Score 473.5;	DB 2;	Length 128;
Best Local Similarity	77.6%	Pred. 0.2, 3e-35;		
Matches 90; Conservative	9;	Mismatches 14;	Indels 3;	Gaps 1;

QY 2 ESGPGLVPSQTLSLTCTVSGSIRSGGYWMSVRQPPKGLEINIGNIYHSGNTYPNPSL 61
| | | | : | | | | | | | | | | | | | | | | | | | | | |
DbB 13 ESGPGLVPSQTLSLTCTVSGSISGGFYWSMIRDHGMALEINIAHITFSGITYNPFL 72

Qy	62	KSRLTMSVDTSEKNHFSRLTSTVAADTAVYYCAR	---	SDGVTLDNNQGGLTVTVSS	114
		::: :	:		
Db	73	KSRLVTSVDTSENOFSLRLTSTVPADTAVYYCAR	IGYNFGYFDPNGCGGLTVTVSS		128

RESULT 11

Ig heavy chain V region (VH4DJH6) - human (Fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence revision 12-Apr-1996 #text change 20-Jun-2000

A:Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 463.5; DB 2; Length 155;
Best Local Similarity 73.3%; Pred. No. 2e-34;
Matches 88; Conservative 12; Mismatches 11; Indels 9; Gaps 2;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVWVROPPGKGLMIGNIYHSGNTYYNPSTL 61
Db 38 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVWVROPPGKGLMIGNIYHSGNTYYNPSTL 95
QY 62 KSRITMSVDTSKNHFSLRLTSTADTAADTAAYVYCARSDG-----YTLDMWGQGLTVVSS 114
Db 96 KSRVTISVDTSKNHFSLRLTSTADTAADTAADTAAYVYCARSDG-----YTLDMWGQGLTVVSS 155

Search completed: August 30, 2006, 00:42:54
Job time : 10.7091 sec

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GenCore version 5.1.9
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OM protein - protein search, using sw model1

Run on: August 30, 2006, 00:29:05 ; Search time 62.1818 Seconds
(without alignments)
1695.862 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 IESGPGYVXPSTSLTCTV.....RSDGYTIDNWGGTIVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492.5	80.2	476	2	Q6GMX1_HUMAN
2	477	77.7	465	2	Q6GMX6_HUMAN
3	476.5	77.6	492	2	Q7Z374_HUMAN
4	470	76.5	478	2	Q7Z379_HUMAN
5	466	75.9	150	2	Q9S973_HUMAN
6	466	75.9	496	2	Q96KX8_HUMAN
7	463.5	75.5	119	2	Q9UL73_HUMAN
8	457	74.4	477	2	Q6GMX7_HUMAN
9	457	74.4	620	2	Q96EY0_HUMAN
10	451	73.5	576	2	Q6PAI8_HUMAN
11	440.5	71.7	129	1	HV2F_HUMAN
12	429	69.9	139	2	Q81D7_HUMAN
13	427	69.5	139	2	Q86SX2_HUMAN
14	426.5	69.5	595	2	Q8WTUX4_HUMAN
15	426.5	69.5	597	2	Q6GMX5_HUMAN
16	426.5	69.5	597	2	Q9BUI0_HUMAN
17	426.5	69.5	625	2	Q96AA6_HUMAN
18	422.5	68.8	597	2	Q9BQ8_HUMAN
19	417.5	68.0	478	2	Q6NYH3_HUMAN
20	417	67.9	146	1	HV2I_HUMAN
21	413	67.3	473	2	Q8TC63_HUMAN
22	386	62.9	116	2	Q7Z3Y6_HUMAN
23	383.5	62.5	476	2	Q6MXZ7_HUMAN
24	383	62.4	483	2	Q5U413_HUMAN
25	382.5	62.3	479	2	Q99M22_MOUSE
26	381.5	62.1	117	1	HV2G_HUMAN
27	377	61.4	136	2	Q6ABQ5_MOUSE
28	375.5	61.2	615	2	Q569B6_RAT
29	371.5	60.5	477	2	Q510J1_RAT
30	365.5	59.5	119	2	Q53VR3_MOUSE
31	365	59.4	122	2	Q9UL75_HUMAN

32	363.5	59.2	137	1	HV46_MOUSE
33	360.5	58.7	115	2	Q53VQ1_MOUSE
34	360.5	58.7	262	2	Q65Z11_MOUSE
35	359.5	58.6	590	2	Q569B8_RAT
36	355.5	57.9	119	2	Q53VQ5_MOUSE
37	355	57.8	485	2	Q56IM5_MOUSE
38	353	57.5	617	2	Q569B3_RAT
39	352.5	57.4	144	1	HV43_MOUSE
40	351	57.2	120	2	Q53VR7_MOUSE
41	347.5	56.6	113	1	HV47_MOUSE
42	347	56.5	591	2	Q510D9_RAT
43	346.5	56.4	121	2	Q9UL96_HUMAN
44	344.5	56.1	469	2	Q5M839_RAT
45	344.5	56.1	485	2	Q58E54_MOUSE

ALIGNMENTS

RESULT 1
Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 19-JUL-2004, integrated into UniProtKB/TREMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: BC073773; AAH73773.1; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KM SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 80.2%; Score 492.5; DB 2; Length 476;
 Best Local Similarity 74.2%; Pred. No. 6.4e-42;
 Matches 92; Conservative 13; Mismatches 6; Indels 13; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWVROPFGKGLWIGNIYHSGNTYNPSTL 61
 DB 25 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWVROPFGKGLWIGNIYHSGNTYNPSTL 84
 QY 62 KSRITWSVDTSKNHSRLTSVTAADTAVYYCARSDGTYLDMWGQTLTV 110
 DB 85 KSRITWSVDTSKNHSRLTSVTAADTAVYYCARSDGTYLDMWGQTLTV 142
 QY 111 TVSS 114
 DB 143 TVSS 146

RESULT 2

06GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
 ID 06GMX6_HUMAN
 AC 06GMX6;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Sculter G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datsenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bork S.A., Loughran N.A., Peters G.J., Abramson R.D., Mullenbach S.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska J., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903 (2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; BC073766; AAH73766.1; -; mRNA.
 DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IG; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KM SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 77.7%; Score 477; DB 2; Length 465;
 Best Local Similarity 81.4%; Pred. No. 2.5e-40;
 Matches 92; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWVROPFGKGLWIGNIYHSGNTYNPSTL 61
 DB 25 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWVROPFGKGLWIGNIYHSGNTYNPSTL 82
 QY 62 KSRITWSVDTSKNHSRLTSVTAADTAVYYCARSDGTYLDMWGQTLTV 114
 DB 83 KSRITWSVDTSKNHSRLTSVTAADTAVYYCARSDGTYLDMWGQTLTV 135

RESULT 3

07Z374_HUMAN PRELIMINARY; PRT; 492 AA.
 ID 07Z374_HUMAN
 AC 07Z374;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Hypothetical protein DKFZp686C02218 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human rectum tumor;
 RA Bloecher H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fodor G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; BX538077; CAD98001.1; -; mRNA.
 DR HSP; P01820; IG7J.
 DR SWP; Q7Z374; 262-470.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IG; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein; Immunoglobulin domain; Repeat.
 KM NON TER 1
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760FCA74B CRC64;

Query Match 77.6%; Score 476.5; DB 2; Length 492;
 Best Local Similarity 76.9%; Pred. No. 2.9e-40;
 Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWVWVROPKGLMIGNIYHSGNTYVPSL 61
 DB 37 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWVWVROPKGLMIGNIYHSGNTYVPSL 96
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR---SDGYTLDMNGGTLTVTSS 114
 DB 97 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARVHGEFGYGFDPWGGGTLTVTSS 152

RESULT 4
 Q72379 HUMAN PRELIMINARY; PRT; 478 AA.
 AC 072379;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Hypothetical protein DKFZp686K04218 (Fragment).
 GN Name=DKFZp686K04218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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EMBL: BX538066; CAY97996.1; -; mRNA.
 DR HSSP; P01820; 1G7J.
 DR SMR; Q72379; 248-456.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig C1.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00407; Ig C1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig Like; 4.
 DR PROSITE; PS00290; Ig MHC; UNKNOWN 2.
 KW Hypothetical protein; Immunoglobulin domain; Repeat.
 FT NON TER 1
 SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 76.5%; Score 470; DB 2; Length 478;
 Best Local Similarity 75.7%; Pred. No. 1,3e-39;
 Matches 87; Conservative 14; Mismatches 12; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWVWVROPKGLMIGNIYHSGNTYVPSL 61
 DB 24 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWVWVROPKGLMIGNIYHSGNTYVPSL 83
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGY--TLDMNGGTLTVTSS 114
 DB 84 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARVHGEFGYGFDPWGGGTLTVTSS 138

RESULT 5
 Q95973 HUMAN PRELIMINARY; PRT; 150 AA.
 AC 095973;
 DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1999, sequence version 1.

DT 07-FEB-2006, entry version 23.
 DE VH4 heavy chain variable region precursor (Fragment).
 GN Name=IGH;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sun C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
 RT "Clonal proliferation of IGM secreting B cell in the synovium of
 RT Behcet's patient with arthritis."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

EMBL: AP103795; AAC79084.1; -; mRNA.
 DR PIR; S31673; S31673.
 DR PIR; S78056; S78056.
 DR HSSP; P01820; 1G7J.
 DR SMR; Q95973; 20-147.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig V.
 DR InterPro; IPR013106; V-set.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig Like; 1.
 KW Immunoglobulin domain; Signal.
 FT SIGNAL 1
 FT CHAIN 20
 FT NON TER 150
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 150;
 Best Local Similarity 76.1%; Pred. No. 9.5e-40;
 Matches 86; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWVWVROPKGLMIGNIYHSGNTYVPSL 61
 DB 25 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWVWVROPKGLMIGNIYHSGNTYVPSL 84
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLTVTSS 114
 DB 85 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARLGKGAEDFGHGTMVTSS 137

RESULT 6
 Q96KX8 HUMAN PRELIMINARY; PRT; 496 AA.
 AC 096KX8;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE WGC27165 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

CC TISSUE=lung;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Mortrud A., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Caavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.W.,
 RA Butcherfield Y.S., Krzywinski M.I., Skalska U., Smallie D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 CC -----
 CC EMBL; BC016369; AAH16369.1; -; mRNA.
 DR HSSP; P01876; IOM0.
 DR SMr; Q96KX8; 266-474.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR003599; IG_1-like.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGC1; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKOWN 1.
 DR PROSITE; PS00290; IG_MHC; UNKOWN 1.
 SO SEQUENCE 496 AA; 53392 MW; D316929849040D69 CRC64;

OC Homo. TaxID=9606;
 RX NCBI_TaxID=9606;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=90578875; PubMed=160528; DOI=10.1084/jem.174.6.1639;
 RA Manheimer-Loy A., Katz J.B., Pillinger M., Grossein C., Smith A.,
 RA Diamond B.;
 RA "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idotype";
 RL J. Exp. Med. 174:1639-1652(1991).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=90059975; PubMed=2511001;
 RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
 RA "The smaller human VH gene families display remarkably little
 RT polymorphism";
 RL EMBO J. 8:3741-3748(1989).
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 CC
 CC EMBL; AF035041; AAD56277.1; -, mRNA.
 DR PIR; PH0876; PH0876.
 DR PIR; S12416; S12416.
 DR HSSP; P01820; 1G7J.
 DR SMR; Q9UL73; 2-119.
 DR LinkHub; Q9UL73; -
 DR InterPro; IPR003599; IG_
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR013106; V-set.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin domain
 KW NON_TER 1
 KW NON_TER 1
 FT 119 119
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EABE CRC64;
 Query Match 75.5%; Score 463.5; DB 2; Length 119;
 Best Local Similarity 77.6%; Pred. No. 1.3e-39;
 Matches 90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;
 QY 2 ESGPGLVKSQTSLLTCTVSGSIRSGGYWVRPPGKLEWIGNIYHSGNTYNPST 61
 DB 6 ESGPGLVKSQTSLLTCTVSGSIRSGGYWVRPPGKLEWIGNIYHSGNTYNPST 63
 QY 62 KSRITMSVDSKHNPSRLTSTVTADPAVYVCAASDG---YTLNMGQGLTVTSS 114
 DB 64 KSRVITISVDRKSNQPSLKLITSLPADRAVFCARLSMWGPIYFPYWGQGLTVTSS 119
 RESULT 8
 OG6MX7 HUMAN
 ID OG6MX7 HUMAN PRELIMINARY; PRT; 477 AA.
 AC OG6MX7;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DE 07-FEB-2006, entry version 16.
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 NCBI_TaxID=9606;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RN Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL Strausberg R.,
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 CC -----
 DR EMBL: BC073765; AA073765.1; -; mRNA.
 DR SMR: Q6GMX7; 247-455.
 DR Ensemble: ENSG00000130076; Homo sapiens.
 DR InterPro: IPR003593; IG.
 DR InterPro: IPR007110; IG_1ike.
 DR InterPro: IPR003597; IG_1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.
 DR Pfam: PF07654; Cl-set; 2.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00407; IG1; 2.
 DR PROSITE: PS50835; IG_1ike; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 477 AA; 51631 MW; 9F59C09C50CFF85 CRC64;
 Query Match 74.4%; Score 457; DB 2; Length 477;
 Best Local Similarity 77.4%; Pred. No. 2, 9e-38;
 Matches 89; Conservative 7; Mismatches 15; Indels 4; Gaps 2;
 QY 2 ESGPGLVKSQTLSTCTVSGSGISRGYVWVROPKGLMIGNIYHSGTYNPSL 61
 DB 25 ESGPGLVKSQTLSTCTVSGSGISS--YVMSIRQTAGLGMIGIYISGSGTYNPSL 82
 QY 62 KSRITNSVDTSKNHSILRLTSVTAADTAVYYCARSDG--YTLDDNGQGLIVTVSS 114
 DB 83 KSRVTLSTLTJKNQFSLRLNSVTAAADTAVYYCAHSGSWDPFAFDYWGQGLIVTVSS 137
 RESULT 9
 Q96EYO HUMAN PRELIMINARY; PRT; 620 AA.
 AC Q96EYO;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 2.
 DT 07-FEB-2006, entry version 26.
 DE IGHM protein.
 GN Name=IGHM;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91252286; PubMed=1904154;
 RA Neale G.A., Kitchingman G.R.;
 RT "RNA transcripts initiating within the human immunoglobulin mu heavy
 RT chain enhancer region contain a non-translatable exon and are
 RL extremely heterogeneous.";
 RL Nucleic Acids Res. 19:2427-2433(1991).
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 CC -----
 DR EMBL: BC011857; AA011857.2; -; mRNA.
 DR PIR: S15590; S15590.
 DR HSSP: P01820; 1G7J.
 DR SMR: Q96EYO; 27-251.
 DR Ensemble: ENSG00000130076; Homo sapiens.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1ike.
 DR InterPro: IPR003597; IG_1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.
 DR Pfam: PF07654; Cl-set; 4.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00407; IG1; 3.
 DR PROSITE: PS50835; IG_1ike; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 620 AA; 68125 MW; 99D1AA6B6FF27B CRC64;
 Query Match 74.4%; Score 457; DB 2; Length 620;
 Best Local Similarity 78.0%; Pred. No. 3, 9e-38;
 Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;
 QY 2 ESGPGLVKSQTLSTCTVSGSGISRGYVWVROPKGLMIGNIYHSGTYNPSL 61
 DB 32 ESGPGLVKSQTLSTCTVSGSGISS--YVMSIRQTAGLGMIGIYISGSGTYNPSL 89

OY KSRITMSVDTSKNHFSLRTSVTADTAVYYCARSDGTLTLDN-----WGQGLTVTVSS 114
 DB 90 KSRVTVSDVTSKQFSLKLSVTADTAVYYCA-SQWELPFTVGLFTWGQGLTVTVSS 146

RESULT 10

06P418_HUMAN PRELIMINARY; PRT; 576 AA.
 ID 06P418_HUMAN
 AC 06P418
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 21-FEB-2006, entry version 20.
 DE IGHAD protein.
 GN Name=IGHD;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marins K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stampleton M., Soares W.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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OY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVROPKGLGEMIGNIYHSGNTYVPSL 61
 DB 32 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVROPKGLGEMIGNIYHSGNTYVPSL 90

OY 62 KSRITMSVDTSKNHFSLRTSVTADTAVYYCARSDG---YTLDNWGQGLTVTVSS 114
 DB 91 KSRVTVSDVTSKQFSLKLSVTADTAVYYCASLDIYYGMDVWGQGLTVTVSS 146

RESULT 11

HV2F_HUMAN STANDARD; PRT; 129 AA.
 ID HV2F_HUMAN
 AC P01824;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 07-MAR-2006, entry version 36.
 DE Ig heavy chain V-II region WHH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Telaar D., Debure B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 RT immunoglobulin D."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma
 CC protein.
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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DR PIR; A02099; D2HUMA.
 DR PDB; 1ZVO; X-ray; C/D=--
 DR SMR; P01824; 2-129.
 DR GlycoSiteDB; P01824; --
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003623; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; Ig-like-
 DR InterPro; IPR003596; Ig v
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT CHAIN 1
 FT DOMAIN 1
 FT NON_TER 129
 FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.7%; Score 440.5; DB 1; Length 129;
 Best Local Similarity 65.1%; Pred. No. 3,4e-37;
 Matches 82; Conservative 14; Mismatches 15; Indels 15; Gaps 2;

OY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVROPKGLGEMIGNIYHSGNTYVPSL 61
 DB 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVROPKGLGEMIGNIYHSGNTYVPSL 65
 OY 62 KSRITMSVDTSKNHFSLRTSVTADTAVYYCARSDG---YTLDNWGQGLTVTVSS 114
 DB 66 KSRVTVSDVTSKQFSLKLSVTADTAVYYCARSDG---YTLDNWGQGLTVTVSS 123
 OY 109 LVTYSS 114

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 / Search time 15.5455 Seconds
(without alignments)
641.891 Million cell updates/sec

Title: US-10-027-725a-8

Perfect score: 614
Sequence: 1 LBSPGLVPRSQTLSTLCTV.....RSDGYTLDMWGGLTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents_AA:*
2: /EMC Celerra_SIDS3/prodata/2/iaa/5 COMB.pep:*
3: /EMC Celerra_SIDS3/prodata/2/iaa/6 COMB.pep:*
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7: /EMC Celerra_SIDS3/prodata/2/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507	82.6	473	2	US-09-049-672A-4
2	504.5	82.2	117	2	US-10-330-613A-13
3	494	80.5	122	1	US-08-360-125-11
4	494	80.5	122	1	US-08-450-578-11
5	494	80.5	122	1	US-09-017-628-11
6	494	80.5	122	1	US-09-014-880-11
7	494	80.5	122	2	US-08-450-363-11
8	494	80.5	122	2	US-09-467-903-11
9	494	80.5	172	2	US-09-472-087-7
10	494	80.5	172	2	US-09-472-087-86
11	493.5	80.4	117	2	US-10-330-613A-5
12	490.5	79.9	117	2	US-09-720-493-2
13	488.5	79.6	119	2	US-09-025-7698-39
14	488.5	79.6	119	2	US-09-025-7698-65
15	488.5	79.6	119	2	US-09-490-070A-39
16	488.5	79.6	119	2	US-09-490-070A-65
17	488.5	79.6	119	2	US-09-490-153-39
18	488.5	79.6	119	2	US-09-490-153-65
19	488.5	79.6	119	2	US-09-490-324-39
20	488.5	79.6	119	2	US-09-490-324-65
21	488	79.5	118	2	US-09-025-7698-25
22	488	79.5	118	2	US-09-490-070A-25
23	488	79.5	118	2	US-09-490-153-25
24	488	79.5	118	2	US-09-490-324-25
25	487.5	79.4	119	2	US-10-330-613A-25
26	482.5	78.6	121	2	US-10-330-613A-37

27	480.5	78.3	117	2	US-10-330-613A-33	Sequence 33, Appl
28	478	77.9	487	2	US-09-800-729-145	Sequence 145, Appl
29	477	77.7	120	2	US-09-424-840B-20	Sequence 20, Appl
30	473.5	77.1	119	1	US-08-360-125-5	Sequence 5, Appl
31	473.5	77.1	119	1	US-08-450-578-5	Sequence 5, Appl
32	473.5	77.1	119	1	US-09-017-628-5	Sequence 5, Appl
33	473.5	77.1	119	1	US-09-014-880-5	Sequence 5, Appl
34	473.5	77.1	119	2	US-08-450-363-5	Sequence 5, Appl
35	473.5	77.1	119	2	US-09-467-903-5	Sequence 5, Appl
36	468.5	76.3	121	2	US-10-330-613A-9	Sequence 9, Appl
37	467.5	76.1	121	2	US-10-330-613A-17	Sequence 17, Appl
38	467.5	76.1	121	2	US-10-330-613A-17	Sequence 17, Appl
39	459.5	74.8	142	1	US-08-480-774A-2	Sequence 2, Appl
40	458	74.6	244	2	US-08-918-148-79	Sequence 79, Appl
41	458	74.6	244	2	US-09-138-091A-77	Sequence 77, Appl
42	455	74.1	99	2	US-10-194-975-38	Sequence 38, Appl
43	454.5	74.0	125	2	US-10-432-006-1	Sequence 1, Appl
44	454	73.9	230	2	US-10-194-975-110	Sequence 110, App
45	453	73.8	99	2	US-10-194-975-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: PANCYTUT01
CLONE: 1513264
US-09-049-672a-4

Query Match 82.6%; Score 507; DB 2; Length 473;
Best Local Similarity 79.8%; Pred. No. 1.1e-42;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYYSWVRQPPGKGLWIGNIYHSGNTYVNSL 61
DB 25 ESGPGLVPSQTLSTCTVSGGSIIRSGYYSWVRQPPGKGLWIGNIYHSGNTYVNSL 84
QY 62 KSRITNSVDTSKQHFSLRTSVTAADTAAYVYCARSD-----GYTLDNMGQGLTVTVSS 114
DB 85 KSRVTTISVDTSKQFSLKLSVTADTAAYVYCARDDVGLRGNGYGMADVWGQGLTVTVSS 143

RESULT 2

US-10-330-613A-13
Sequence 13, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330.613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match 82.2%; Score 504.5; DB 2; Length 117;
Best Local Similarity 84.2%; Pred. No. 3.8e-43;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYYSWVRQPPGKGLWIGNIYHSGNTYVNSL 61
DB 6 ESGPGLVPSQTLSTCTVSGGSIIRSGYYSWVRQPPGKGLWIGNIYHSGNTYVNSL 65
QY 62 KSRITNSVDTSKQHFSLRTSVTAADTAAYVYCARSDGYTLDNMGQGLTVTVSS 114
DB 66 KSRVTTISVDTSKQFSLKLSVTADTAAYVYCARDDVGLRGNGYGMADVWGQGLTVTVSS 117

RESULT 3

US-08-360-125-11
Sequence 11, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:

INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

ORGANELLE:
IMMEDIATE SOURCE:

LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:

MAP POSITION:
UNITS:
FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:

PUBLICATION INFORMATION:
AUTHORS:
TITLE:

JOURNAL:
VOLUME:
ISSUE:
PAGES:

DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-11

Query Match 80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.5e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYYSWVRQPPGKGLWIGNIYHSGNTYVNSL 61
DB 6 ESGPGLVPSQTLSTCTVSGGSIIRSGYYSWVRQPPGKGLWIGNIYHSGNTYVNSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYYCARSD-----GYTLDMNGGGLTVTVSS 114
Db 66 KSRVITISVDTSKNHFSLRLTSVTAADTAIVYYCARSGTGGYYTGMDDWGQGLTVTVSS 122

RESULT 4

US-08-450-578-11
Sequence 11, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845hiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450, 578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:

POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:

DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.5e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQSLTCTVSGGSIIRSGYVSWVROPKGLMIGNIYHSGNTYVPSL 61
Db 6 ESGPGLVKSQSLTCTVSGGSIIRSGYVSWVROPKGLMIGNIYHSGNTYVPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYYCARSD-----GYTLDMNGGGLTVTVSS 114
Db 66 KSRVITISVDTSKNHFSLRLTSVTAADTAIVYYCARSGTGGYYTGMDDWGQGLTVTVSS 122

RESULT 5

US-09-017-628-11
Sequence 11, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Yoshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287hiko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017, 628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 122
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match 80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.5e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQSLTCTVSGGSIIRSGYVSWVROPKGLMIGNIYHSGNTYVPSL 61
Db 6 ESGPGLVKSQSLTCTVSGGSIIRSGYVSWVROPKGLMIGNIYHSGNTYVPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYYCARSD-----GYTLDMNGGGLTVTVSS 114
Db 66 KSRVITISVDTSKNHFSLRLTSVTAADTAIVYYCARSGTGGYYTGMDDWGQGLTVTVSS 122


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1  AUTHORS:
2  TITLE:
3  JOURNAL:
4  VOLUME:
5  ISSUE:
6  PAGES:
7  DATE:
8  DOCUMENT NUMBER:
9  FILING DATE:
10 PUBLICATION DATE:
11 RELEVANT RESIDUES IN SEQ ID NO:
12
13 US-08-450-363-11

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Query Match          80.5%:  Score 494;  DB 2;  length 122;
Best Local Similarity 78.6%:  Pred. No. 4, 5e-42;
Matches    92;  Conservative    10;  Mismatches    11;  Indels    4;  Gaps    1;

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QY 2 ESQGLVLPSPQTSLTCTVSGGSIIRSGGYWMSWVRPGKGLGMIININYSGLTYNPGL 61
Db 6 ESQGLVLPSPQTSLTCTVSGGSIIRSGGYWMSWVRPGKGLGMIININYSGLTYNPGL 65
QY 62 KSRTTMSVYHSKHFSLRLTSVTAADPAVYVCARSD---GYLDMNGGTLTVYS 114
Db 66 KSRVTSVYHSKQFSLKLSSTVTAADPAVYVCARGSGGYTGMDWVGQSTVTVYS 122

RESULT 8
US-09-467-903-11

```

; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA

```

No. 6787153hiko ITO
 Kazuhiko NAGAIKE
 TITLE OF INVENTION: Human Monoclonal Antibody
 Specifically Binding to Surface Antigen of Cancer
 Cell Membrane

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendrooth, Lind & Ponack
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

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PRIOR APPLICATION DATA:
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: 08/450,363
FILING DATE: MAY 25, 1995
APPLICATION NUMBER: 08/360,125

1 FILED: JUNE 29, 1992
2 FILING DATE: June 29, 1992
3 APPLICATION NUMBER: JP158859/1991
4 FILING DATE: June 28, 1991
5 APPLICATION NUMBER: JP158860/1991
6 FILING DATE: June 28, 1991
7 APPLICATION NUMBER: JP158861/1991

```

;
; ATTORNEY/AGENT INFORMATION:
;
;   NAME: Wai'ten M. Cheek Jr.
;   REGISTRATION NUMBER: 33,367
;   REFERENCE/DOCKET NUMBER: <Unknown>
;

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TELECOMMUNICATION INFORMATION
TELEPHONE: 202-721-8200
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS

LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROTHERICAL: <unknown>
ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:

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1 INDIVIDUAL ISOLATE: <Unknown>
2
3 DEVELOPMENTAL STAGE: <Unknown>
4
5 HAPLOTYPE: <Unknown>
6
7 TISSUE TYPE: <Unknown>
8
9 CELL TYPE: Hybridoma producing human antibody 1-3-1

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? IMMEDIATE SOURCE:
? LIBRARY: <unknown>
? CLONE: <unknown>
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: <unknown>
?

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NAME/KEY :
LOCATION :
IDENTIFICATION METHOD:
OTHER INFORMATION :
PUBLICATION INFORMATION:

;	PUBLICATION DATE:	
;	RELEVANT RESIDUES IN SEQ ID NO:	
;	SEQUENCE DESCRIPTION: SEQ ID NO:	11:
;		
US-09-467-903-11		

Query Match	80.5%	Score 494;	DB 2;	Length 122;
Best Similarity	78.6%	Pred. No. 4	5e-42;	
Best Local	92;	Conservative	11;	Indels 4;
Matches				Gaps 1.

QY 2 EGGPGLYVKRSQTLSLTCTVSGSSSSGGGYGSMVWQPKPKGLWMTGNTHSGNTYNNPGL 61
Db 6 EGGPGLYVKRSSETLSLTCTVSGSSISSSTYMGWIKRQPKGLGHEIMGISTYYSGSTYNNPGL 65
QY 62 KSRITMSVDTSKNHFSLRITSYTAADTAVYYCARSD---GTTLDNGGGLTYVSS 114
Db 66 KSRVITSVDTSKNOFSLKLSSTVADTAVYYCARGGYGGYGGMDWGGLTYVSS 122

RESULT 9
US-09-47

Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVU, MARK J.
APPLICANT: MUELLER, RILEN E.
APPLICANT: HANKE, JEFFERY H.
APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY
TITLE OF INVENTION: CORVALLAN, JOSE R.
FILE REFERENCE: ABX-PPI
CURRENT APPLICATION NUMBER: US/09/472.087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-7

Query Match 80.5%; Score 494; DB 2; Length 172;
Best Local Similarity 81.6%; Pred. No. 6,7e-42;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 3 SGGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSLK 62
DB 1 SGGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSLK 60
QY 63 SRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDMWGQGLTVTVSS 114
DB 61 SRVTISVDTSKNQFSKLSSVTAADTAVYYCARSDGSDYGIIDVWGQGLTVTVSS 114

RESULT 10
US-09-472-087-86
Sequence 86, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MODELIER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALLAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPI
CURRENT APPLICATION NUMBER: US/09/472.087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match 80.5%; Score 494; DB 2; Length 172;
Best Local Similarity 81.6%; Pred. No. 6,7e-42;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 3 SGGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSLK 62
DB 1 SGGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSLK 60
QY 63 SRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDMWGQGLTVTVSS 114
DB 61 SRVTISVDTSKNQFSKLSSVTAADTAVYYCARSDGSDYGIIDVWGQGLTVTVSS 114

RESULT 11
US-10-330-613A-5
Sequence 5, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:

APPLICANT: Guigas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-5

Query Match 80.4%; Score 493.5; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 4,8e-42;
Matches 95; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 2 ESGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSL 61
DB 6 ESGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGTLDMWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSKLSSVTAADTAVYYCARSDGSDYGIIDVWGQGLTVTVSS 117

RESULT 12
US-09-720-493-2
Sequence 2, Application US/09720493
Patent No. 6827925
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holte, Thor L
APPLICANT: Main, Sarah H
APPLICANT: Jackson, Helen
APPLICANT: Darmanis, Olayekan
TITLE OF INVENTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CP5775333
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-720-493-2

Query Match 79.9%; Score 490.5; DB 2; Length 117;
Best Local Similarity 81.4%; Pred. No. 9,6e-42;
Matches 92; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 2 ESGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSL 61
DB 6 ESGPLVKSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNTYHSGNTYNNPSL 64
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDMWGQGLTVTVSS 114
DB 65 KSRVTISVDTSKNQFSKLSSVTAADTAVYYCARSDGSDYGIIDVWGQGLTVTVSS 117

RESULT 13
US-09-025-769B-39
Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Laming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-39
Query Match 79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.5e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVROPKGLWMIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVROPKGLWMIGNIYHSGNTYNNPSL 63
QY 62 KSRITWSDTSKXHFSLRLTSVTAADTAVYYCAR--SDG-YTLDDNQGQGLTVTVSS 114
DB 64 KSRVITSDTSKXQFSLKLSVTAADTAVYYCARWGDDGFYADYWGQGLTVTVSS 119
RESULT 14
US-09-025-769B-65
Sequence 65, Application US/09025769B
Patent No. 6300664
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Laming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65
Query Match 79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.5e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVROPKGLWMIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVROPKGLWMIGNIYHSGNTYNNPSL 63
QY 62 KSRITWSDTSKXHFSLRLTSVTAADTAVYYCAR--SDG-YTLDDNQGQGLTVTVSS 114
DB 64 KSRVITSDTSKXQFSLKLSVTAADTAVYYCARWGDDGFYADYWGQGLTVTVSS 119
RESULT 15
US-09-490-070A-39
Sequence 39, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Laming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McCaulliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

```
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39

Query Match      79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.5e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

QY      2  ESGRGLVKPSQTSLTCTVSGSGSTRSGGYVWSWVROPKGLIEWIGNIYHSGNTYVNSL 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      6  ESGRGLVKPSQTSLTCTVSGSGSTRSGGYVWSWVROPKGLIEWIGNIYHSGNTYVNSL 63

QY      62  KSRITMSVDTSKNHPSRLTSTVADTAIVYYCAR--SDG-YTLDDMGQGLIVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      64  KSRVTISVDTSKNHPSRLTSTVADTAIVYYCARMGSDGFYANDYWGQGLIVTVSS 119
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Search completed: August 30, 2006, 00:37:09
Job time : 15.5455 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 65.2909 Seconds
(without alignments)
808.788 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	4	US-10-027-725A-8
2	600	97.7	114	4	US-10-027-725A-9
3	546	88.9	114	4	US-10-027-725A-7
4	514.5	83.8	140	5	US-10-893-576-41
5	511	83.2	128	5	US-10-727-155-2
6	511	83.2	128	5	US-10-727-155-10
7	511	83.2	128	5	US-10-727-155-30
8	510.5	83.1	121	4	US-10-309-762-152
9	510	83.1	118	4	US-10-309-762-138
10	509.5	83.0	123	4	US-10-309-762-10
11	507.5	82.7	125	4	US-10-309-762-11
12	507	82.6	120	4	US-10-309-762-13
13	507	82.6	120	4	US-10-309-762-14
14	507	82.6	122	4	US-10-309-762-147
15	506.5	82.5	119	5	US-10-893-576-189
16	506	82.4	221	3	US-09-972-656-80
17	505.5	82.3	121	4	US-10-309-762-151
18	505	82.2	128	5	US-10-727-155-26
19	504.5	82.2	117	4	US-10-330-613-13
20	504.5	82.2	117	4	US-10-330-613-13
21	504.5	82.2	117	4	US-10-660-357-13
22	504	82.1	121	5	US-10-805-177-56
23	503.5	82.0	119	4	US-10-309-762-140
24	503.5	82.0	148	6	US-11-131-648-13
25	503.5	82.0	148	6	US-11-131-648-35
26	503	81.9	125	5	US-10-805-177-53
27	502.5	81.8	123	4	US-10-309-762-12

28	502.5	81.8	144	5	US-10-893-576-35	Sequence 35, Appl
29	502	81.8	122	5	US-10-984-960A-56	Sequence 56, Appl
30	502	81.8	124	5	US-10-309-762-75	Sequence 75, Appl
31	502	81.8	143	4	US-10-309-762-96	Sequence 96, Appl
32	501	81.6	130	6	US-11-009-731-46	Sequence 46, Appl
33	501	81.6	222	3	US-09-880-748-1329	Sequence 1329, Ap
34	501	81.6	252	4	US-10-293-418-1329	Sequence 1329, Ap
35	501	81.6	252	6	US-11-054-515-1329	Sequence 1329, Ap
36	501	81.6	252	6	US-11-266-444-1329	Sequence 1329, Ap
37	500	81.4	120	4	US-10-309-762-128	Sequence 128, Ap
38	500	81.4	120	4	US-10-309-762-139	Sequence 139, Ap
39	500	81.4	121	4	US-10-308-817-137	Sequence 137, Ap
40	500	81.4	121	4	US-10-453-698-137	Sequence 137, Ap
41	500	81.4	126	3	US-09-974-449-6	Sequence 6, Appl
42	500	81.4	126	5	US-10-652-502A-18	Sequence 18, Appl
43	499.5	81.4	135	4	US-10-388-214A-34	Sequence 34, Appl
44	499	81.3	116	4	US-10-309-762-127	Sequence 127, Appl
45	499	81.3	120	5	US-10-706-689-40	Sequence 40, Appl

ALIGNMENTS

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RESULT 1
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-8

Query Match      100.0%; Score 614; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 9, 3e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYWSWVQPPKGLWIGNIYHSGNTYVPS 60
      |||||
Db      1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYWSWVQPPKGLWIGNIYHSGNTYVPS 60
      |||||

QY      61 LKSRITMSVDTSKNHFSLRTSTYAADTAVYYCARSDGYTLDMWGQGLVTVSS 114
      |||||
Db      61 LKSRITMSVDTSKNHFSLRTSTYAADTAVYYCARSDGYTLDMWGQGLVTVSS 114
      |||||

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
```



```
/
/
/ APPLICANT: Jaspal S. Kang
/ APPLICANT: Orit Record
/ APPLICANT: Larry Green
/ APPLICANT: Xiao Feng
/ APPLICANT: Scott Klakamp
/ APPLICANT: Mary Haak-Frendescho
/ APPLICANT: Palaniswami Rathanaswami
/ APPLICANT: Craig Figott
/ APPLICANT: Meina Liang
/ APPLICANT: Rozanne Lee
/ APPLICANT: Kathy Manchulenko
/ APPLICANT: Raffaella Faggioni
/ APPLICANT: Giorgio Senaldi
/ APPLICANT: Qiaojuan Jane Su
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
/ TITLE OF INVENTION: FACTOR AND USES THEREOF
/ FILE REFERENCE: ABGENIX.073A
/ CURRENT APPLICATION NUMBER: US/10/727,155
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/430729
/ NUMBER OF SEQ ID NOS: 320
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-727-155-10
```

```
Query Match 83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 2,1e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPKGLWIGNIYSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPKGLWIGNIYSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTAVYYCARSDG-----YTLDMNGGGLTVT 111
DB 66 KSRVITISVDTSKNHSRLTSTVTAADTAVYYCARSDGNDVYDGLDVGGGTTVT 125
```

```
QY 112 VSS 114
DB 126 VSS 128
```

```
RESULT 7
US-10-727-155-30
/ Sequence 30, Application US/10727155
/ Publication No. US20050049402A1
/ GENERAL INFORMATION:
/ APPLICANT: John S. Babcock
/ APPLICANT: Jaspal S. Kang
/ APPLICANT: Orit Record
/ APPLICANT: Larry Green
/ APPLICANT: Xiao Feng
/ APPLICANT: Scott Klakamp
/ APPLICANT: Mary Haak-Frendescho
/ APPLICANT: Palaniswami Rathanaswami
/ APPLICANT: Craig Figott
/ APPLICANT: Meina Liang
/ APPLICANT: Rozanne Lee
/ APPLICANT: Kathy Manchulenko
/ APPLICANT: Raffaella Faggioni
/ APPLICANT: Giorgio Senaldi
/ APPLICANT: Qiaojuan Jane Su
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
/ TITLE OF INVENTION: FACTOR AND USES THEREOF
/ FILE REFERENCE: ABGENIX.073A
/ CURRENT APPLICATION NUMBER: US/10/727,155
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/430729
/ PRIOR FILING DATE: 2002-12-02
```

```
/ NUMBER OF SEQ ID NOS: 320
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-727-155-30
```

```
Query Match 83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 2,1e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPKGLWIGNIYSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPKGLWIGNIYSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTAVYYCARSDG-----YTLDMNGGGLTVT 111
DB 66 KSRVITISVDTSKNHSRLTSTVTAADTAVYYCARSDGNDVYDGLDVGGGTTVT 125
```

```
QY 112 VSS 114
DB 126 VSS 128
```

```
RESULT 8
US-10-309-762-152
```

```
/ Sequence 152, Application US/10309762
/ Publication No. US20040018198A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Gudas, Jean
/ APPLICANT: Folz, Ian
/ APPLICANT: Handa, Masahisa
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
/ FILE REFERENCE: ABGENIX.027A
/ CURRENT APPLICATION NUMBER: US/10/309,762
/ PRIOR FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: 60/337275
```

```
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 152
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-309-762-152
```

```
Query Match 83.1%; Score 510.5; DB 4; Length 121;
Best Local Similarity 82.8%; Pred. No. 2,2e-38;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPKGLWIGNIYSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPKGLWIGNIYSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTAVYYCARSDG-----GYTLDMNGGGLTVT 114
DB 66 KSRVITISVDTSKNHSRLTSTVTAADTAVYYCARSDGNDVYDGLDVGGGTTVT 121
```

```
RESULT 9
US-10-309-762-138
/ Sequence 138, Application US/10309762
/ Publication No. US20040018198A1
/ GENERAL INFORMATION:
/ APPLICANT: Gudas, Jean
/ APPLICANT: Folz, Ian
/ APPLICANT: Handa, Masahisa
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
/ TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

```
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138
```

```
Query Match      83.1%; Score 510; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 2,4e-38;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 2 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYNPSTL 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGYIYSGSTYNPSTL 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGTYLDNMGCGTLVTYSS 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARYYSGSDYWGQGLVTYSS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 10

```
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Handa, Masahisa
; APPLICANT: Foltz, Ian
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
```

```
Query Match      83.0%; Score 509.5; DB 4; Length 123;
Best Local Similarity 82.2%; Pred. No. 2,7e-38;
Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;
```

```
QY 2 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYNPSTL 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGYIYSGSTYNPSTL 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGTYLDNMGCGTLVTYSS 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARAGKYYGSYLDYWGQGLVTYSS 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 11

```
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
```

```
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11
```

```
Query Match      82.7%; Score 507.5; DB 4; Length 125;
Best Local Similarity 81.7%; Pred. No. 4,2e-38;
Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
```

```
QY 2 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYNPSTL 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGYIYSGNTYNPSTL 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGTYLDNMGCGTLVTYSS 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARYYDFLTGYPAFDIMGQGTWTVSS 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 12

```
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13
```

```
Query Match      82.6%; Score 507; DB 4; Length 120;
Best Local Similarity 83.6%; Pred. No. 4,5e-38;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
```

```
QY 2 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYNPSTL 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGVLVPSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGYIYSGSTYNPSTL 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGTYLDNMGCGTLVTYSS 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARSDGTYLDNMGCGTLVTYSS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 13

```
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
```


;; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
;; FILE REFERENCE: (CA IX) TUMOR ANTIGEN
;; CURRENT APPLICATION NUMBER: US/10/309,762
;; PRIOR FILING DATE: 2002-12-02
;; PRIOR FILING DATE: 2001-12-03
;; NUMBER OF SEQ ID NOS: 246
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 144
;; LENGTH: 120
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match 82.6%; Score 507; DB 4; Length 120;
Best Local Similarity 83.6%; Pred. No. 4.5e-38;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVRPPGKGLWMIGNIYHSGNTYYNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVRPPGKGLWMIGNIYHSGNTYYNPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYT---LDNMGQGLTVTVSS 114
DB 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYT---LDNMGQGLTVTVSS 120

RESULT 14
US-10-309-762-147
;; Sequence 147, Application US/10309762
;; Publication No. US20040018198A1
;; GENERAL INFORMATION:
;; APPLICANT: Gudas, Jean
;; APPLICANT: Foltz, Ian
;; APPLICANT: Handa, Masahisa
;; APPLICANT: Gallo, Michael
;; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
;; FILE REFERENCE: ABGENIX.027A
;; CURRENT APPLICATION NUMBER: US/10/309,762
;; CURRENT FILING DATE: 2002-12-02
;; PRIOR FILING DATE: 2001-12-03
;; NUMBER OF SEQ ID NOS: 246
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 147
;; LENGTH: 122
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-309-762-147

Query Match 82.6%; Score 507; DB 4; Length 122;
Best Local Similarity 82.1%; Pred. No. 4.5e-38;
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVRPPGKGLWMIGNIYHSGNTYYNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVRPPGKGLWMIGNIYHSGNTYYNPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYT---LDNMGQGLTVTVSS 114
DB 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYT---LDNMGQGLTVTVSS 122

RESULT 15
US-10-893-576-189
;; Sequence 189, Application US/10893576
;; Publication No. US20050118643A1
;; GENERAL INFORMATION:
;; APPLICANT: BURGESS, TERESA L.
;; APPLICANT: COXON, ANGELA
;; APPLICANT: GREEN, LARRY L.

;; APPLICANT: ZHANG, KE
;; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
;; FILE REFERENCE: 06843.0051-00000
;; CURRENT APPLICATION NUMBER: US/10/893,576
;; PRIOR FILING DATE: 2004-07-16
;; PRIOR FILING DATE: 2003-07-18
;; NUMBER OF SEQ ID NOS: 194
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 189
;; LENGTH: 119
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic gamma heavy
US-10-893-576-189

Query Match 82.5%; Score 506.5; DB 5; Length 119;
Best Local Similarity 84.2%; Pred. No. 4.9e-38;
Matches 96; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVRPPGKGLWMIGNIYHSGNTYYNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVRPPGKGLWMIGNIYHSGNTYYNPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYT---LDNMGQGLTVTV 112
DB 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYT---LDNMGQGLTVTV 119

Search completed: August 30, 2006, 00:50:39
Job time : 66.2909 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 13.4727 Seconds
(without alignments)
578.960 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLTVVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /IMC_Celerra_SIDS3/prodata/2/pubppaa/US09_NEW_PUB.pep:*
- 2: /IMC_Celerra_SIDS3/prodata/2/pubppaa/US06_NEW_PUB.pep:*
- 3: /IMC_Celerra_SIDS3/prodata/2/pubppaa/US07_NEW_PUB.pep:*
- 4: /IMC_Celerra_SIDS3/prodata/2/pubppaa/US08_NEW_PUB.pep:*
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- 6: /IMC_Celerra_SIDS3/prodata/2/pubppaa/US10_NEW_PUB.pep:*
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- 8: /IMC_Celerra_SIDS3/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	510.5	83.1	118	6	US-10-981-300-51	Sequence 51, App1
2	488.5	79.6	119	7	US-11-304-986-25	Sequence 25, App1
3	487.5	79.4	149	7	US-11-355-464-13	Sequence 13, App1
4	487.5	79.4	149	7	US-11-355-464-16	Sequence 16, App1
5	485.5	79.1	118	6	US-10-981-300-52	Sequence 52, App1
6	485.5	79.1	180	6	US-10-981-300-4	Sequence 4, App1
7	483.5	78.7	121	7	US-11-337-300-84	Sequence 84, App1
8	483.5	78.7	248	7	US-11-337-300-94	Sequence 94, App1
9	481.5	78.4	121	7	US-11-211-917-82	Sequence 82, App1
10	481.5	78.4	121	7	US-11-211-917-98	Sequence 98, App1
11	481.5	78.4	466	7	US-11-211-917-86	Sequence 70, App1
12	481.5	78.4	466	7	US-11-211-917-86	Sequence 86, App1
13	479.5	78.1	121	7	US-11-211-917-66	Sequence 66, App1
14	478	77.9	118	7	US-11-211-917-109	Sequence 109, App1
15	478	77.9	118	7	US-11-211-917-142	Sequence 142, App1
16	478	77.9	120	7	US-11-281-266-6	Sequence 6, App1
17	475	77.4	126	6	US-10-981-300-53	Sequence 53, App1
18	475	77.4	126	6	US-10-994-679-68	Sequence 68, App1
19	473	77.0	120	7	US-11-211-917-108	Sequence 108, App1
20	471.5	76.8	121	7	US-11-211-917-26	Sequence 26, App1
21	471.5	76.8	466	7	US-11-211-917-30	Sequence 30, App1
22	470.5	76.6	119	7	US-11-211-917-18	Sequence 18, App1
23	470.5	76.6	464	7	US-11-211-917-22	Sequence 22, App1
24	469	76.4	108	7	US-11-281-266-82	Sequence 82, App1
25	468.5	76.3	121	6	US-10-994-679-60	Sequence 60, App1

26	465.5	75.8	107	6	US-10-484-105-18	Sequence 18, App1
27	465	75.7	108	7	US-11-281-266-85	Sequence 85, App1
28	464	75.6	244	7	US-11-317-786B-17	Sequence 17, App1
29	464	75.6	448	7	US-11-317-786B-9	Sequence 9, App1
30	462.5	75.3	118	6	US-10-981-300-54	Sequence 54, App1
31	462.5	75.3	443	6	US-10-981-300-20	Sequence 20, App1
32	460.5	75.0	113	7	US-11-290-687-17	Sequence 17, App1
33	460	74.9	247	6	US-10-539-402-10	Sequence 10, App1
34	458.5	74.7	127	7	US-11-259-133-202	Sequence 202, App1
35	458	74.6	244	7	US-11-402-010-77	Sequence 77, App1
36	457	74.4	244	7	US-11-317-786B-19	Sequence 19, App1
37	457	74.4	448	7	US-11-317-786B-11	Sequence 11, App1
38	456	74.3	240	7	US-11-317-786B-15	Sequence 15, App1
39	456	74.3	445	7	US-11-317-786B-32	Sequence 32, App1
40	456	74.3	448	7	US-11-317-786B-7	Sequence 7, App1
41	453	73.8	118	7	US-11-281-266-42	Sequence 42, App1
42	453	73.8	286	7	US-11-154-103-8	Sequence 8, App1
43	451	73.5	112	7	US-11-249-296-64	Sequence 64, App1
44	451	73.5	138	7	US-11-171-085-8	Sequence 8, App1
45	451	73.5	245	6	US-10-539-402-16	Sequence 16, App1

ALIGNMENTS

RESULT 1
US-10-981-300-51
Sequence 51, Application US//10981300
Publication No. US20060093599A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
TITLE OF INVENTION: FOR MAKING AND USING THE SAME
FILE REFERENCE: ABGX-005
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-981-300-51

Query Match 83.1%; Score 510.5; DB 6; Length 118;
Best Local Similarity 85.0%; Pred. No. 9.6e-39;
Matches 96; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 2 ESGRGLVKSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYVPSL 61
DB 6 ESGRGLVKSQTLSTCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYVPSL 65
QY 62 KSRVTISVPTSKNHFSLRLTSTVTAADTAVYVCARSDGYTLDMWGQGLTVVSS 114
DB 66 KSRVTISVPTSKNHFSLRLTSTVTAADTAVYVCARSDGYTLDMWGQGLTVVSS 117

RESULT 2
US-11-304-986-25
Sequence 25, Application US//11304986
Publication No. US20060165682A1
GENERAL INFORMATION:
APPLICANT: Wyeth and Neuraltab et al.
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
FILE REFERENCE: EBN-055
CURRENT APPLICATION NUMBER: US/11/304,986
CURRENT FILING DATE: 2005-12-15
PRIOR APPLICATION NUMBER: 60/636684
PRIOR FILING DATE: 2004-12-15
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct, consensus sequence for heavy chain
; OTHER INFORMATION: framework region
US-11-304-986-25

Query Match      79.6%; Score 488.5; DB 7; Length 119;
Best Local Similarity 81.9%; Pred. No. 8.8e-37;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Qy      2  ESGPGLVPSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNIYHSGNTYVPSL 61
Db      6  ESGPGLVPSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNIYHSGNTYVPSL 63

Qy      62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCAR--SDG-YTLDMWGQGLVTVSS 114
Db      64 KSRVTVSDTSKNQFSLKLSSTVTAADTAIVYYCARWGDDGFYAMDYWGQGLVTVSS 119

RESULT 3
US-11-355-464-13
; Sequence 13, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall1
; APPLICANT: CHALLITA-ElD, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US/11/355,464
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-355-464-13

Query Match      79.4%; Score 487.5; DB 7; Length 149;
Best Local Similarity 78.5%; Pred. No. 1.3e-36;
Matches 95; Conservative 8; Mismatches 9; Indels 9; Gaps 2;
```

```
Qy      114 S 114
Db      123 S 123

RESULT 4
US-11-355-464-16
; Sequence 16, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall1
; APPLICANT: CHALLITA-ElD, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US/11/355,464
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-355-464-16

Query Match      79.4%; Score 487.5; DB 7; Length 149;
Best Local Similarity 78.5%; Pred. No. 1.3e-36;
Matches 95; Conservative 8; Mismatches 9; Indels 9; Gaps 2;

Qy      2  ESGPGLVPSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNIYHSGNTYVPSL 61
Db      4  ESGPGLVPSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNIYHSGNTYVPSL 63

Qy      62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCARSDGYT-----LDNMWGQGLVTVSS 113
Db      64 KSRVTVSDTSKNQFSLKLSSTVTAADTAIVYYCAR-DHITWVRGVPKMDVWGQGLVTVSS 122

Qy      114 S 114
Db      123 S 123

RESULT 5
US-10-981-300-52
; Sequence 52, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
```

CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-981-300-52

Query Match 79.1%; Score 485.5; DB 6; Length 118;
Best Local Similarity 81.4%; Pred. No. 1,6e-36;
Matches 92; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 61
DB 6 QGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 65

QY 62 KSRITMSVDTSKNHSRLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVYSS 114
DB 66 KSRFTISVDTSKNQPSLKLSTVTAADTAVYYCARTGDY-FDYWGQGLTVYSS 117

RESULT 6

US-10-981-300-4
Sequence 4, Application US/10981300
Publication No. US20060093599A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
APPLICANT: GADI GAJIT-BORNSTEIN
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
FILE REFERENCE: ABQY-005
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 180
TYPE: PRT
ORGANISM: homo sapien
US-10-981-300-4

Query Match 79.1%; Score 485.5; DB 6; Length 180;
Best Local Similarity 81.4%; Pred. No. 2.4e-36;
Matches 92; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 61
DB 6 QGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 65

QY 62 KSRITMSVDTSKNHSRLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVYSS 114
DB 66 KSRFTISVDTSKNQPSLKLSTVTAADTAVYYCARTGDY-FDYWGQGLTVYSS 117

RESULT 7

US-11-337-300-84
Sequence 84, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
APPLICANT: ter Meulen, Jan H.
APPLICANT: De Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudemil, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
SEQ ID NO 84

LENGTH: 121
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Variable heavy chain of SC03-017
US-11-337-300-84

Query Match 78.7%; Score 483.5; DB 7; Length 121;
Best Local Similarity 80.0%; Pred. No. 2.5e-36;
Matches 92; Conservative 11; Mismatches 9; Indels 3; Gaps 2;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 61
DB 8 EGGAGILKPSQTLSTLCTVSGSVSGSYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 67

QY 62 KSRITMSVDTSKNHSRLRLTSVTAADTAVYYCA--RSDGYTLDMWGQGLTVYSS 114
DB 68 KSRVITSDVTSKNQPSLKLSTVTAADTAVYYCAKRSAGF-FDYWGQGLTVYSS 121

RESULT 8

US-11-337-300-94
Sequence 94, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: De Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudemil, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
SEQ ID NO 94
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: SC03-017
US-11-337-300-94

Query Match 78.7%; Score 483.5; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 5e-36;
Matches 92; Conservative 11; Mismatches 9; Indels 3; Gaps 2;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 61
DB 9 EGGAGILKPSQTLSTLCTVSGSVSGSYVSWVRQPPKGLEWIGNIYHSGNTYYPSTL 68

QY 62 KSRITMSVDTSKNHSRLRLTSVTAADTAVYYCA--RSDGYTLDMWGQGLTVYSS 114
DB 69 KSRVITSDVTSKNQPSLKLSTVTAADTAVYYCAKRSAGF-FDYWGQGLTVYSS 122

RESULT 9

US-11-211-917-82
Sequence 82, Application US/11211917
Publication No. US20060093600A1
GENERAL INFORMATION:
APPLICANT: BEIDIAN, VAHE
APPLICANT: GLADIE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR APPLICATION NUMBER: US/10/292,088
PRIOR FILING DATE: 2002-11-08

```

: PRIOR APPLICATION NUMBER: 60/348,980
: PRIOR FILING DATE: 2001-11-09
: NUMBER OF SEQ ID NOS: 147
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 82
: LENGTH: 121
: TYPE: PRT
: ORGANISM: Homo sapiens
: OS-11-211-917-82

```

Query Match	78.4%	Score	481.5	DB	7	Length	121
Best Local Similarity	79.7%	Pred.	No. 3.8e-36				
Matches	94	Conservative	8	Mismatches	9	Indels	7
						Gaps	2

```

QY      2  ESGPGLVKPSQSLSTCTVSGGSRSGGYYSWVRQPPGKGLBNINIHSGNTYINPSL 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      6  ESGPGLVKPSLSTCTVSGGSR--GYYSWVRQPPGKGLWICYIYSGSTNNPSL 63

```

```

Qy      62 KSRITMSVDTSKNHFSRLTSLVTADTAVVYCARSDGYTLDD----NMGGITLVVSS 114
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      64 KSRVTISVDTSKNQFSLKLTSSVTADTAVVYCARGGELYGDYGMFAPMGGLTVVSS 121

```

```

US-11-211-917-98
RESULT 10
; Sequence 98, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 121
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-211-917-98

```

Query Match	78.4%	Score 481.5	DB 7	Length 121
Best Local Similarity	79.7%	Pred. No. 3.8e-36		
Matches 94, Conservative		7, Mismatches 10,	Indels 7,	Gaps 2,

QY 2 ESAGELVPSQTLILITCVSGSIRSGGYYSWVROPFGKLEWIGIYHSNUNYPSL 6
Db 6 ESGRLVPSFETLSITCVSGSIR--GYYSWVIRPPGKLEWIGIYHSSTNNYPSL 6
QY 62 KSRITMSVDTSKNNHSEFLRITVTLADNAVYCARSDGTYLD----NWGGILVYWS 114
Db 64 KSRVITSDVTSKNNFSLKNSVTGLADNAVYCARKGIGYGDYGAFAPWGGTGLTVWS 121

RESULT11
 US-11-211-917-70
 : Sequence 70, Application US/11211917
 : Publication No. US20060093600A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: BEDITA, VAHE
 : APPLICANT: GLADBE, RONALD P.
 : APPLICANT: CORVALLAN, JOSE
 : APPLICANT: JIA, XIAO-CHI
 : APPLICANT: FENG, XIAO
 :
 : TITLE OF INVENTION: ANTIBODIES TO CD40

```

; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-211-917-70

```

Query Match	78.4%	Score 481.5	DB 7	Length 466
Best Local Similarity	79.7%	Pred. No. 1.4e-35		
Matches 94; Conservative	7	Mismatches 10	Indels 7	Gaps 2

QY 2 ESAGGLVKKPQOTLSTLTCTVSGGSGIRSGCYWMSVWRP PGKGLGEMININIHSGMTYNNPSL 62
Db 25 ESAGGLVKKPQETLSTLTCTVSGGSGIR--GYWMSIRQPGKGLGEMITGYIYSSSTNNPSL 82
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYYCARSDGYILD----NMGGTLVYIYSS 114
Db 83 KSRITLISVDTSKNHFSLKLSVTAADTAIVYYCARSGGLGVDGWFAPMGOGTILVYSS 140

```

US-11-211-917-86
RESULT12
; Sequence 86, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,911
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 866
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-211-917-86

```

Query Match	78.4%;	Score	481.5;	DB	7;	Length	466;
Best Local Similarity	79.7%;	Pred. NO.	1.4e-35;				
Matches	94;	Conservative	8;	Mismatches	9;	Indels	7;
						Gaps	2

QY	2	ESGGGLVXPSCOTSLILCTCGAGGSRSGGYGYSWVRPGKGLGEMINILNHYSGATYNNPSL	61
Db	25	ESGGGLVXPSCSTLSLICTVAGGSR--GYTMSMIRPGKGLGEMIGLYYSSGSTNNPSL	8
QY	62	KSRLTMSYDYSKHFSLRLISVTAADPAVYVCARSDGYTLD-----NMGGTLVYSS	114
Db	83	KSRLTISYDYSKDFSLKLSVTAADPAVYVCARGGLYGDYGFAPMGGGTLVATSS	140

RESULT 13
US-11-211-917-66
; Sequence 66, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE

```
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: PENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ CURRENT FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 66
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-211-917-66
```

```
Query Match          78.1%; Score 479.5; DB 7; Length 121;
Best Local Similarity 79.7%; Pred. No. 5.7e-36;
Matches 94; Conservative 6; Mismatches 11; Indels 7; Gaps 2;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCCARSDGYTLD----NMGGGTLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAADTAAYYCCARSDGYTLDYGMFAPMGGTLVTYSS 121
```

```
RESULT 14
US-11-211-917-109
/ Sequence 109, Application US/11211917
/ Publication No. US20060093600A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VAHE
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: PENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ CURRENT FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 109
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-211-917-109
```

```
Query Match          77.9%; Score 478; DB 7; Length 118;
Best Local Similarity 80.9%; Pred. No. 7.5e-36;
Matches 93; Conservative 8; Mismatches 10; Indels 4; Gaps 2;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCCARSDGYTLD--LNMGGGTLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAADTAAYYCCARSDGYTLDYGMFAPMGGTLVTYSS 118
```

RESULT 15

```
US-11-211-917-142
/ Sequence 142, Application US/11211917
/ Publication No. US20060093600A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VAHE
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: PENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PF/3 US
/ CURRENT APPLICATION NUMBER: US/11/211,917
/ CURRENT FILING DATE: 2005-08-25
/ PRIOR APPLICATION NUMBER: US/10/292,088
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 142
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-211-917-142
```

```
Query Match          77.9%; Score 478; DB 7; Length 118;
Best Local Similarity 81.7%; Pred. No. 7.5e-36;
Matches 94; Conservative 8; Mismatches 9; Indels 4; Gaps 3;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCCARSDGYT--LNMGGGTLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAADTAAYYCCARSDGYTLDYGMFAPMGGTLVTYSS 118
```

Search completed: August 30, 2006, 00:52:02
Job time : 13.4727 secs

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PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT	variable region of group 2 allergen specific-human IgE Fabs, useful for
PT	diagnosing or passive immunotherapy of type I allergy, for environmental
PT	allergen detection.
PS	
PS	Disclosure; Page 36; 45pp; English.
XX	
CC	This invention relates to the DNA and protein sequences of group 2
CC	allergen-specific human IgE Fabs and methods for their use. The proteins
CC	of the invention may have antiallergic activities and may be used as a
CC	vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC	antibodies to Phi p 2 (a major Timothy grass pollen allergen). The group
CC	2 allergen-specific fabs of the invention may be useful for environmental
CC	allergen detection and for standardization of allergen extracts. The fabs
CC	or a vaccine against a type I allergy is useful for passive
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type
CC	I allergy. The allergen-specific fabs of the invention are useful for
CC	in vivo diagnosis, therapy and prevention of type I allergy. They are
CC	also useful for identification of group 2 allergen-containing pollen and
CC	may be used for blocking the binding of grass pollen allergic patients
CC	IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC	fab, clone 94 heavy chain protein of the invention
XX	
XX	Sequence 114 AA;
XX	
Query Match	100.0%; Score 609; DB 5; Length 114;
Best Local Similarity	100.0%; Pred. No. 3.7e-48;
Matches 114; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 LESGPGLYKPAQTLSLSCAVSGSGSIRSGGYWSMIRHPGKLEWIGYIHSGNTYNP
DB	1 LESGPGLYKPAQTLSLSCAVSGSGSIRSGGYWSMIRHPGKLEWIGYIHSGNTYNP
OY	61 LKSRFAMSVDTSENKPSRLINSVTAADPAVYVYCAALDGGTTLIDIMOGGTLVTWSS
OY	61 LKSRFAMSVDTSENKPSRLINSVTAADPAVYVYCAALDGGTTLIDIMOGGTLVTWSS
DB	61 LKSRFAMSVDTSENKPSRLINSVTAADPAVYVYCAALDGGTTLIDIMOGGTLVTWSS
RESULT 2	
ABG30447	
ID	ABG30447 standard; protein; 114 AA.
XX	ABG30447;
XX	
DT	21-OCT-2002 (first entry)
XX	
DE	Human IgE Fab clone 100 heavy chain protein.
XX	
XX	Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KW	climchy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..26
FT	/note= "FR1 region"
FT	27..33
FT	/note= "CD1 region"
FT	34..47
FT	/note= "FR2 region"
FT	48..63
FT	/note= "CD2 protein"
FT	64..95
FT	/note= "FR3 region"
FT	96..103
FT	/note= "CD2 region"
FT	104..114
FT	/note= "FR4 region"
XX	
XX	WO200253595-A1.
XX	
PD	11-JUL-2002.
XX	

PF	27-DEC-2001; 2001WO-SE002908.	
PR	29-DEC-2000; 2000SE-00004892.	
XX		
XX	(PHAA) PHARMACIA DIAGNOSTICS AB.	
PA		
PI	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX		
DR	WPI: 2002-583604/62.	
XX	N-PSDB; ABK89639.	
XX		
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising	
PT	variable region of group 2 allergen specific-human IgE Fabs, useful for	
PT	diagnosing or passive immunotherapy of type I allergy, for environmental	
PT	allergen detection.	
XX		
PS	Disclosure; Page 38; 45pp; English.	
XX		
CC	This invention relates to the DNA and protein sequences of group 2	
CC	allergen-specific human IgE Fabs and methods for their use. The proteins	
CC	of the invention may have antiallergic activities and may be used as a	
CC	vaccine or an inhibitor of binding of grass pollen allergic patient's IgE	
CC	antibodies to Phi P 2 (a major timothy grass pollen allergen). The group	
CC	2 allergen-specific Fabs of the invention may be useful for environmental	
CC	allergen detection and for standardisation of allergen extracts. The Fabs	
CC	- or a vaccine againsts a type I allergy is useful for passive	
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type	
CC	I allergy. The allergen-specific Fabs of the invention are useful for	
CC	inter alia, diagnosis, therapy and prevention of type I allergy. They are	
CC	also useful for identification of group 2 allergen-containing pollen and	
CC	may be used for blocking the binding of grass pollen allergic patients	
CC	IgE antibodies to Phi P 2. The present sequence represents the human IgG	
CC	fab, clone 100 heavy chain protein of the invention	
XX		
SO	Sequence 114 AA:	
Query Match	89.8%; Score 547; DB 5; Length 114;	
Best Local Similarity	89.5%; Pred. No. 1.8e-42;	
Matches 102; Conservative	5; Mismatches 7; Indels 0; Gaps 0;	
OY	1 LESGPGVLKPKPQOTLSLSCAVSGSGSIRSGGYWSWIRQHPGKGLMWIGYIHSGNTYYNPS 60	
DB	1 LESGPGVLKPKPQOTLSLTCVSGSIRSGGYWSWIRQHPGKGLMWIGYIHSGNTYYNPS 60	
OY	61 LKSRIAMSVPTSENKPSIRLNSVTADTAVYYCARLDGYTLIDWGQTLVTWSS 114	
DB	61 LKSRIAMSVPTSENKPSIRLNSVTADTAVYYCARLDGYTLIDWGQTLVTWSS 114	
RESULT 3		
ABG30446		
ID	ABG30446 standard; protein; 114 AA.	
XX		
AC	ABG30446;	
XX		
DT	21-OCT-2002 (first entry)	
DE		
XX	Human IgE Fab clone 60 heavy chain protein.	
XX		
KW	Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;	
XX	timothy grass pollen allergen; passive immunotherapy.	
OS		
XX	Homo sapiens.	
FH		
FT	Key	Location/Qualifiers
FT	Region	1..26
FT	Region	/note= "FR1 region"
FT	Region	27..33
FT	Region	/note= "CDR1 region"
FT	Region	34..47
FT	Region	/note= "FR2 region"
FT	Region	48..63
FT	Region	/note= "CDR2 protein"

FT Region 64..95
 FT /note="PR3 region"
 FT Region 96..103
 FT /note="CDR2 region"
 FT Region 104..114
 FT /note="PR4 region"
 PN WO200253595-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 27-DEC-2001; 2001WO-SE002908.
 XX
 PR 29-DEC-2000; 2000SE-00004892.
 XX
 PA (PHMA) PHARMACIA DIAGNOSTICS AB.
 PI Flicker S, Steinberger P, Kraft D, Valenta R;
 XX
 DR WPI; 2002-583604/62.
 XX
 DR N-PSDB; ABK89638.
 XX
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.
 PS
 PS Disclosure; Page 37; 45pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
 CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific Fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The Fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy. It is also useful for diagnosing a type
 CC I allergy. The allergen-specific Fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergenic patient's
 CC IgE antibodies to Phi P 2. The present sequence represents the human IgG
 CC Fab, clone 60 heavy chain protein of the invention
 XX
 SQ Sequence 114 AA;
 XX
 Query Match 89.7%; Score 546; DB 5; Length 114;
 Best Local Similarity 89.5%; Pred. No. 2.3e-42;
 Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 LESGPGLVKPAQTLISLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSGNTYNNPS 60
 DB 1 LESGPGLVKPSQTLISLCTVSGSIRSGGYWMIROHPKGLGEMIGYIHSGNTYNNPS 60
 QY 61 LKSRIMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLIDWGGQTLVTSS 114
 DB 61 LKSRITMSVDTSKNFSRLNSVTAADTAVYCARLDGYTLIDWGGQTLVTSS 114
 XX
 RESULT 4
 ADP03977 ID ADP03977 standard; protein; 122 AA.
 XX
 AC ADP03977;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
 XX
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 XX
 PN WO2003048328-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 02-DEC-2002; 2002WO-US038550.
 XX
 PR 03-DEC-2001; 2001US-0337275P.
 XX
 PA (ABGE-) ABGENIX INC.
 PI Gudas J, Poltz I, Handa M, Gallo M;
 XX
 DR WPI; 2003-523295/49.
 XX
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 PS
 PS Example 2; SEQ ID NO 147; 89pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 XX
 SQ Sequence 122 AA;
 XX
 Query Match 85.2%; Score 519; DB 7; Length 122;
 Best Local Similarity 81.2%; Pred. No. 7.3e-40;
 Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;
 QY 2 ESGPGLVKAQTLISLSCAVSGSIRSGGYWMIROHPKGLGEMIGYIHSGNTYNNPSL 61
 DB 6 ESGPGLVKPSQTLISLCTVSGSIRSGGYWMIROHPKGLGEMIGYIHSGNTYNNPSL 65
 QY 62 KSRIMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLIDWGGQTLVTSS 114
 DB 66 KSRITMSVDTSKNFSRLNSVTAADTAVYCARLDGYTLIDWGGQTLVTSS 122
 XX
 RESULT 5
 ADP03982 ID ADP03982 standard; protein; 121 AA.
 XX
 AC ADP03982;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
 XX
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 XX
 PN WO2003048328-A2.

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XX 12-JUN-2003.
PD
XX
XX 02-DEC-2002; 2002MO-US038550.
PF
XX
XX 03-DEC-2001; 2001US-0337275P.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX Gudae J, Foltz I, Handa M, Gallo M;
PI
XX WPI; 2003-523295/49.
DR
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 152; 89pp; English.
PS
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolastic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 121 AA:
SQ

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Query Match      85.1%; Score 518.5; DB 7; Length 121;
Best Local Similarity 81.9%; Pred. No. 8.1e-40;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 2 ESGPGLVKPAQTSLSCAVSGSIRSGGYWMIROHPGKGLFEMIGIYHSGNTYNPSTL 61
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 6 ESGPGLVKPQSTLCTVSGSISGGYWSWIRHPGKGLFEMIGIYHSGNTYNPSTL 65
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 62 KSRIRMSVDTSENKFSRLNSVTAPADTAVYYCARLD---GYTLDIWGQTLVTYSS 114
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 66 KSRITISVDTSKNQFSLKLSSTVTAADTAVYYCAVYDILTGAYDIMGQTMVTYSS 121
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 6
ADP03871
ID ADP03871 standard; protein; 125 AA.
XX
XX ADP03871;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
DE
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolastic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX
XX WO2003048328-A2.
PN
XX
XX 12-JUN-2003.
PD
XX
XX 02-DEC-2002; 2002MO-US038550.
PF
XX
XX 03-DEC-2001; 2001US-0337275P.
PR

```

```

XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudae J, Foltz I, Handa M, Gallo M;
PI
XX
XX WPI; 2003-523295/49.
DR
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 11; 89pp; English.
PS
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolastic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 125 AA:
SQ

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```

Query Match      85.0%; Score 517.5; DB 7; Length 125;
Best Local Similarity 81.7%; Pred. No. 1e-39;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

QY 2 ESGPGLVKPAQTSLSCAVSGSIRSGGYWMIROHPGKGLFEMIGIYHSGNTYNPSTL 61
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 6 ESGPGLVKPQSTLCTVSGSISGGYWSWIRHPGKGLFEMIGIYHSGNTYNPSTL 65
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 62 KSRIRMSVDTSENKFSRLNSVTAPADTAVYYCAR----LDGY--TLDIWGQTLVTYSS 114
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 66 KSRITISVDTSKNQFSLKLSSTVTAADTAVYYCARYDYDFLTGYPDAFDIMGQTMVTYSS 125
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 7
ADP03981
ID ADP03981 standard; protein; 121 AA.
XX
XX ADP03981;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 151.
DE
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolastic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX
XX WO2003048328-A2.
PN
XX
XX 12-JUN-2003.
PD
XX
XX 02-DEC-2002; 2002MO-US038550.
PF
XX
XX 03-DEC-2001; 2001US-0337275P.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudae J, Foltz I, Handa M, Gallo M;
PI
XX
XX WPI; 2003-523295/49.
DR

```

```

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
PS
XX Example 2; SEQ ID NO 151; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 121 AA;
Query Match      84.5%; Score 514.5; DB 7; Length 121;
Best Local Similarity 81.0%; Pred. No. 1.9e-39;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;
OY 2 ESGPGLVKAQQTSLSCAVSGGSIKSGGYWMIKHPGKGLWIGYTHSGNTYNPSTL 61
DB 6 ESGPGLVKAQQTSLSCAVSGGSIKSGGYWMIKHPGKGLWIGYTHSGNTYNPSTL 65
OY 62 KSRVITSVDSIKKQFSLKLSSTVTAADTAAYTCARLDMFGIMDVGQGLTVVSS 114
DB 66 KSRVITSVDSIKKQFSLKLSSTVTAADTAAYTCARLDMFGIMDVGQGLTVVSS 121

RESULT 8
ADP03968
ID ADP03968 standard; protein; 118 AA.
XX
AC ADP03968;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytostatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudaa J, Foltz J, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 138; 89pp; English.

```

```

XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 118 AA;
Query Match      84.1%; Score 512; DB 7; Length 118;
Best Local Similarity 83.2%; Pred. No. 3.1e-39;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
OY 2 ESGPGLVKAQQTSLSCAVSGGSIKSGGYWMIKHPGKGLWIGYTHSGNTYNPSTL 61
DB 6 ESGPGLVKAQQTSLSCAVSGGSIKSGGYWMIKHPGKGLWIGYTHSGNTYNPSTL 65
OY 62 KSRVITSVDSIKKQFSLKLSSTVTAADTAAYTCARLDMFGIMDVGQGLTVVSS 114
DB 66 KSRVITSVDSIKKQFSLKLSSTVTAADTAAYTCARLDMFGIMDVGQGLTVVSS 118

RESULT 9
ADP03974
ID ADP03974 standard; protein; 120 AA.
XX
AC ADP03974;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytostatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudaa J, Foltz J, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 144; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

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CC demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

XX
SQ Sequence 120 AA;

Query Match 84.1%; Score 512; DB 7; Length 120;
Best Local Similarity 81.9%; Pred. No. 3.2e-39;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVKPAQTLTSLSCAVSGSIRSGGYWMSIRQHPKGLGEMIGYIHSGNTYNPSTL 61
DB 6 ESGPGLVKPQSQTSLTCTVSGSISGGYWSWIRQHPKGLGEMIGYIYSGSTYNPSTL 65

QY 62 KSRIVSVDTSENKFSRLNSVTADTAVYYCARLDGYT---LDIWQGGTLVTYVSS 114
DB 66 KSRVTTISVDTISKNQFSLKLSSTVTRADTAVYYCAR-DGYNWYWFDMGRGTLVTYVSS 120

RESULT 10
ADP03873 standard; protein; 120 AA.

XX
AC ADP03873;
XX
DT 29-JUL-2004 (first entry)

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.

XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytoskeletal; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.

XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002MO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudaa J, Foltz I, Handa M, Gallo M;
XX
PI WPI; 2003-523295/49.
XX
DR
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX
PS Claim 1; SEQ ID NO 13; 89pp; English.

XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytoskeletal activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

XX
SQ Sequence 120 AA;

Query Match 84.1%; Score 512; DB 7; Length 120;
Best Local Similarity 81.9%; Pred. No. 3.2e-39;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVKPAQTLTSLSCAVSGSIRSGGYWMSIRQHPKGLGEMIGYIHSGNTYNPSTL 61
DB 6 ESGPGLVKPQSQTSLTCTVSGSISGGYWSWIRQHPKGLGEMIGYIYSGSTYNPSTL 65

QY 62 KSRIVSVDTSENKFSRLNSVTADTAVYYCARLDGYT---LDIWQGGTLVTYVSS 114
DB 66 KSRVTTISVDTISKNQFSLKLSSTVTRADTAVYYCAR-DGYNWYWFDMGRGTLVTYVSS 120

RESULT 11
ADP03872 standard; protein; 123 AA.

XX
AC ADP03872;
XX
DT 29-JUL-2004 (first entry)

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 12.

XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytoskeletal; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.

XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002MO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudaa J, Foltz I, Handa M, Gallo M;
XX
PI WPI; 2003-523295/49.
XX
DR
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX
PS Claim 1; SEQ ID NO 12; 89pp; English.

XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytoskeletal activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.

XX
SQ Sequence 123 AA;

Query Match 83.7%; Score 509.5; DB 7; Length 123;

Best Local Similarity 78.8%; Pred. No. 5.5e-39;
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

QY 2 EGGPGIVKPAQTLISCAVSGSIRSGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 61
DB 6 EGGPGIVKPSQTLISLCTVSGSISGGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 65

QY 62 KSRIVMSVDTSENKPSLRINSVTADTAVYYCARL-----DGYTLDIWGQGLVTVSS 114
DB 66 KSRVTVISVDTSENKPSLRINSVTADTAVYYCARVLLMFEDYGVDMVGQGLVTVSS 123

RESULT 12

AE94855
ID AEE94855 standard; protein; 148 AA.

AC AEE94855;

DT 23-FEB-2006 (first entry)

DE Antibody VH region specific for antigen PSCA, SEQ ID: 35.

XX monoclonal antibody; diagnosis; diagnostic; pharmaceutical;
XX drug screening; cell proliferation; cancer; cytostatic; neoplasm; tumor;
XX PSCA; antibody.

XX Homo sapiens.

XX WO2005118864-A2.

XX 15-DEC-2005.

XX 17-MAY-2005; 2005WO-US017412.

XX 28-MAY-2004; 2004US-00857484.

XX 28-MAY-2004; 2004WO-US017231.

XX 05-OCT-2004; 2004US-0616381P.

XX 12-OCT-2004; 2004US-0617881P.

XX 21-OCT-2004; 2004US-0621310P.

XX 02-DEC-2004; 2004US-0633077P.

XX 14-APR-2005; 2005US-0672000P.

XX (AGEN-) AGENSYS INC.

XX Gudae J, Jakobovits A, Jia X, Morrison RK, Morrison KM, Shao H;

XX Challita-Eid PM, Raitano AB;

XX N-PSDB; AEE94854.

XX WPI; 2006-047570/05.

XX New antibody that binds to PSCA protein, useful for diagnosing,

XX prognosing, preventing, and/or treating cancer, e.g. prostate, pancreas,

XX bladder, kidney, colon, lung, ovary, or breast cancer.

XX Disclosure; SEQ ID NO 35; 282zp; English.

XX The new invention relates to antibodies and binding fragments that bind

XX to PSCA proteins. PSCA, referred to as PSCA v.1 in the specification, was

XX identified as an antigen expressed in prostate cancer. Specifically given

XX is an antibody or fragment comprising an antigen-binding site that binds

XX specifically to PSCA protein. Also given are a transgenic animal that

XX produces the monoclonal antibody; a hybridoma that produces the

CC toxin, a therapeutic agent, or a chemotherapeutic agent. The antigen-

CC binding site specifically binds to an epitope within amino acids of a

CC protein comprising any of 21 sequences (SEQ ID NOS: 13-33). The antibody,

CC protein, composition, vaccines, and method are useful for diagnosing,

CC prognosing, preventing, and/or treating cancer. The present sequence is a

CC VH region of an antibody specific for PSCA protein.

XX SQ Sequence 148 AA;

QY 2 EGGPGIVKPAQTLISCAVSGSIRSGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 61

DB 15 EGGPGIVKPSQTLISLCTVSGSISGGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 74

QY 62 KSRIVMSVDTSENKPSLRINSVTADTAVYYCARLDG-----YTLDIWGQGLVTVSS 113

DB 75 KSRVTVISVDTSENKPSLRINSVTADTAVYYCAR-DGIMIRGYGYGMDVMVGQGLVTVSS 133

QY 114 S 114

DB 134 S 134

RESULT 13

AE94833
ID AEE94833 standard; protein; 148 AA.

AC AEE94833;

DT 23-FEB-2006 (first entry)

DE Antibody VH region specific for cancer antigen PSCA, SEQ ID: 13.

XX monoclonal antibody; diagnosis; diagnostic; pharmaceutical;

XX drug screening; cell proliferation; cancer; cytostatic; neoplasm; tumor;

XX PSCA; antibody.

XX Homo sapiens.

XX WO2005118864-A2.

XX 15-DEC-2005.

XX 17-MAY-2005; 2005WO-US017412.

XX 28-MAY-2004; 2004US-00857484.

XX 28-MAY-2004; 2004WO-US017231.

XX 05-OCT-2004; 2004US-0616381P.

XX 12-OCT-2004; 2004US-0617881P.

XX 21-OCT-2004; 2004US-0621310P.

XX 02-DEC-2004; 2004US-0633077P.

XX 14-APR-2005; 2005US-0672000P.

XX (AGEN-) AGENSYS INC.

XX Gudae J, Jakobovits A, Jia X, Morrison RK, Morrison KM, Shao H;

XX Challita-Eid PM, Raitano AB;

XX N-PSDB; AEE94854.

XX WPI; 2006-047570/05.

XX New antibody that binds to PSCA protein, useful for diagnosing,

XX prognosing, preventing, and/or treating cancer, e.g. prostate, pancreas,

CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cyrostatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.

XX
 SQ Sequence 123 AA;

Query Match 83.5%; Score 508.5; DB 7; Length 123;
 Best Local Similarity 80.5%; Pred. No. 6.6e-39;
 Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVKPAQTLISCAVSGSIRSGGYTSMIRHFGKLEWIGYIYHSGNTYYPSTL 61
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 6 ESGPGLVKPESQTLISCTVSGGSINSGYTWMSWIRHFGKLEWIGYIYHSGNTYYPSTL 65
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 62 KSRIAMSVDTSENKFSIRLNSVTADTAATVYTCAR----LDGYTLDIWGQGLVTVSS 114
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 66 KSRVVISVDTSENQFSLKLSSTVTAADTAATVYTCARERTDYRYGLDVMGQGLVTVSS 123
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: August 30, 2006, 00:41:53
 Job time : 103.427 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 10.7091 Seconds
(without alignments)
1024.243 Million cell updates/sec

Title: US-10-027-725A-7

Sequence: 1 LBSGFLVPAQTLSLSCAV.....RLDGYTLDIWGQTLVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479.5	78.7	116	2 S37456	Ig mu chain - huma
2	476.5	78.2	135	2 S78051	Ig heavy chain pre
3	475.5	78.1	128	2 S31514	Ig heavy chain - h
4	465	76.4	122	2 S69912	Ig V-D-J region (N
5	464.5	76.3	147	2 S13519	Ig heavy chain V r
6	460	75.5	130	2 S30534	Ig heavy chain V r
7	458.5	75.3	140	2 I37782	Ig variable region
8	453	74.4	99	2 S26801	Ig heavy chain V r
9	452.5	74.3	146	2 S09710	Ig heavy chain V r
10	451.5	74.1	121	2 S44113	Ig heavy chain V r
11	451.5	74.1	130	2 S31690	Ig heavy chain V r
12	450.5	74.0	127	2 S19668	Ig heavy chain V r
13	450.5	74.0	146	2 S09711	Ig heavy chain V r
14	449.5	73.8	155	2 S31511	Ig heavy chain - h
15	446.5	73.3	155	2 S31512	Ig heavy chain - h
16	444	72.9	137	2 S31676	Ig heavy chain V r
17	440	72.2	139	2 S31586	Ig heavy chain V r
18	439	72.1	145	2 S78051	Ig heavy chain pre
19	436	71.6	99	2 S26803	Ig heavy chain V r
20	435.5	71.5	123	2 S30530	Ig heavy chain V r
21	434	71.3	129	2 S44114	Ig heavy chain V r
22	433.5	71.2	117	2 S34964	Ig heavy chain pre
23	432.5	71.0	109	2 PH1673	Ig heavy chain V r
24	431	70.8	99	2 S26802	Ig heavy chain V r
25	430	70.6	97	2 PL0118	Ig heavy chain V-I
26	430	70.6	99	2 S26899	Ig heavy chain V-I
27	427	70.1	110	2 S44110	Ig heavy chain V-D
28	426	70.0	139	2 A41287	Ig heavy chain pre
29	425.5	69.9	121	2 C55257	Ig gamma heavy cha

30	424	69.6	118	2 A26340	Ig heavy chain pre
31	423	69.5	118	2 S20780	Ig heavy chain V r
32	421.5	69.2	140	2 A49045	Ig heavy chain V r
33	419.5	68.9	129	1 D2HUMA	Ig heavy chain V-I
34	419	68.8	135	2 S31604	Ig heavy chain V r
35	418.5	68.7	99	2 A38911	Ig heavy chain V r
36	418	68.6	99	2 S26807	Ig heavy chain V r
37	417	68.5	115	2 S57464	Ig heavy chain V-D
38	417	68.5	126	2 S47010	Ig heavy chain V-I
39	417	68.5	140	2 S78052	Ig heavy chain pre
40	416.5	68.4	140	2 A24770	hypothetical_hybr1
41	415.5	68.2	143	2 B49028	Ig heavy chain V-I
42	415	68.1	99	2 S12418	Ig heavy chain V r
43	414.5	68.1	137	2 S31585	Ig heavy chain V r
44	414	68.0	120	2 PT0370	Ig mu chain precu
45	412.5	67.7	98	2 S26502	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S37456 Ig mu chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37456 R/McIntosh, R.S.; Tandon, N.; Weetman, A.P.

submitted to the EMBL Data Library, September 1993

A/Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from i

A/Reference number: S37453

A/Accession: S37456

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-116 <MC1>

A/Cross-references: UNIPARC:UP100001161C0; EMBL:X75024; NID:G404313; PIDN:CAA52932.1; PII

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7% ; Score 479.5 ; DB 2 ; Length 116 ;
Best Local Similarity 76.1% ; Pred. No. 7e-38 ;
Matches 89 ; Conservative 14 ; Mismatches 5 ; Indels 9 ; Gaps 2 ;

Qy 6 GLVKAQTSLSCAVGSGSRGSGYWSMTROHPRGKLEWIGYISGNTYVPSLSKSR 65
Db 1 GLVKAQTSLSCAVGSGSRGSGYWSMTROHPRGKLEWIGYISGNTYVPSLSKSRV 60
Qy 66 AMSVDTSSEKFSRLNSVTADTAAYVYCARLDGVT-----LDIWGQTLVTSS 114
Db 61 TISVDTSKQFSLKLSVTADTAAYVYCAR-GGYSYGYYVMDYWGKTTVTSS 116

RESULT 2

S78051 Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051; S23716

R/Harindranath, N.

submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 <HAR>

A/Cross-references: UNIPARC:UP10000115B87; EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID

Int. Harindranath, N.; Goldfarb, I.S.; Ikenatsu, H.; Buxastero, S.E.; Wilder, R.L.; Nockling, A.

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h

patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A/Molecule type: mRNA

A:Residues: 13-111 <HAW>
A:Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:127-111/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 476.5; DB 2; Length 135;
Best Local Similarity 76.3%; Pred. No. 1.6e-37;
Matches 90; Conservative 13; Mismatches 10; Indels 5; Gaps 2;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
DB 18 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 77
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCARL--DGYTL--DIWOGTLVTVSS 114
DB 78 KSRVTVSDTSKNQFSKLKLSVTADTAAYYCARLGPDDYTLDGMDVWGQGLTVTVSS 135

RESULT 3

S31514
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31514
R:Chaetagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31514
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <CHA>
A:Cross-references: UNIPARC:UPI00001160PB; EMBL:X69862; NID:G33086; PIDN:CAA49496.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 475.5; DB 2; Length 128;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
Matches 89; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
DB 13 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 72
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCARL--DGYTL--DIWOGTLVTVSS 114
DB 73 KSRVTVSDTSKNQFSKLKLSVTADTAAYYCARLGPDDYTLDGMDVWGQGLTVTVSS 128

RESULT 4

S69912
Ig V-D-J region (ND) - human
C:Species: Homo sapiens (man)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69912
R:Shohra, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A:Reference number: S69909; MUID:94335315; PMID:8057663
A:Accession: S69912
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SHN>
A:Cross-references: UNIPARC:UPI0000116640; EMBL:Z33398; NID:G871347; PIDN:CAA83849.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 465; DB 2; Length 122;

Best Local Similarity 75.2%; Pred. No. 1.7e-36;
Matches 88; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 65
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCARL--DGYTL--DIWOGTLVTVSS 114
DB 66 KSRVTVSDTSKNQFSKLKLSVTADTAAYYCARLGPDDYTLDGMDVWGQGLTVTVSS 122

RESULT 5

S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MUID:91187691; PMID:2011536
A:Accession: S13519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <MOR>
A:Cross-references: UNIPARC:UPI0000115EB5; EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 464.5; DB 2; Length 147;
Best Local Similarity 75.9%; Pred. No. 2.3e-36;
Matches 88; Conservative 11; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
DB 32 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 91
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCARL--DGYTL--DIWOGTLVTVSS 114
DB 92 KSRVTVSDTSKNQFSKLKLSVTADTAAYYCARLGPDDYTLDGMDVWGQGLTVTVSS 147

RESULT 6

S30534
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C:Accession: S30534
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30534
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <MAR>
A:Cross-references: UNIPARC:UPI0000113F45; EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 460; DB 2; Length 130;
Best Local Similarity 72.8%; Pred. No. 5.3e-36;
Matches 91; Conservative 10; Mismatches 12; Indels 12; Gaps 2;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKAQTLISCAVSGSIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 65
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCARL--DGYTL--DIWOGTLVTVSS 114
DB 66 KSRVTVSDTSKNQFSKLKLSVTADTAAYYCARLGPDDYTLDGMDVWGQGLTVTVSS 122

QY 110 VTSS 114
DB 126 VTSS 130

RESULT 7

137782
Ig variable region (VDJ) (Clone T23-9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: J37782, S25476
R:Demaison, C.; Chataigner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A36876; MUID:94119917; PMID:8290556
A:Accession: J37782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: UNIPARC:UP10000176883; EMBL:X67906; NID:G33582; PIDN:CAA48104.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 458.5; DB 2; Length 140;
Best Local Similarity 75.4%; Pred. No. 7.9e-36;
Matches 89; Conservative 12; Mismatches 10; Indels 7; Gaps 2;

QY 2 BSGPGLVPAQTLSTLSCAVSGSIRSGYWSWIRHPGKGLWIGIYTHSGNTYNNPSL 61
DB 25 BSGPGLVKSPTSLTCTVSGSGISS--YYWSWIRQPPGKGLWIGIYTHSGNTYNNPSL 82

QY 62 KSRIMSVDTSENKSLRLNSVTAAADTAAYYCARLDG-----GYTLDMGQGLTVTSS 114
DB 83 KSRVITSDTKNSPGLKLSVTAADTAAYYCARHNSSSWYGYPFDYWGQGLTVTSS 140

RESULT 8

S26801
Ig heavy chain V region (DP-65) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C:Accession: S26801, S26900
R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A:Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26801
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <MEN>
A:Cross-references: UNIPARC:UP10000116419; EMBL:Z14237; NID:G37706; PIDN:CAA78606.1; PID
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <TOM>
A:Cross-references: UNIPARC:UP10000116419; EMBL:Z12365; NID:G32948; PIDN:CAA78235.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 453; DB 2; Length 99;
Best Local Similarity 86.2%; Pred. No. 1.8e-35;
Matches 81; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 2 BSGPGLVPAQTLSTLSCAVSGSIRSGYWSWIRHPGKGLWIGIYTHSGNTYNNPSL 61
DB 6 BSGPGLVKSPTSLTCTVSGSGISSGYYWSWIRHPGKGLWIGIYTHSGNTYNNPSL 65

QY 62 KSRIMSVDTSENKSLRLNSVTAAADTAAYYCAR 95
DB 66 KSRVITSDTKNSPGLKLSVTAADTAAYYCAR 99

RESULT 9

S09710
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A:Reference number: S09710; MUID:90262535; PMID:2111699
A:Accession: S09710
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <HUG>
A:Cross-references: UNIPARC:UP100011586C; GB:X52110; NID:G31447; PIDN:CAA36344.1; PID:G
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 452.5; DB 2; Length 146;
Best Local Similarity 68.3%; Pred. No. 3e-35;
Matches 84; Conservative 16; Mismatches 12; Indels 11; Gaps 2;

QY 2 BSGPGLVPAQTLSTLSCAVSGSIRSGYWSWIRHPGKGLWIGIYTHSGNTYNNPSL 61
DB 25 BSGPGLVKSPTSLTCTVSGSVSGGLYWGVRQPPGKGLWIGIYTHSGNTYNNPSL 84

QY 62 KSRIMSVDTSENKSLRLNSVTAAADTAAYYCARLDG-----TLDMGQGLTVT 111
DB 85 KSRVITSDTKNSPGLKLSVTAADTAAYYCTR-PGIGDTSVRKRWMMDLMGQGLTVT 143

QY 112 VSS 114
DB 144 VSS 146

RESULT 10

S44113
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44113
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A:Reference number: S44105
A:Accession: S44113
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <HAM>
A:Cross-references: UNIPARC:UP100011662F; EMBL:Z31389; NID:G472967; PIDN:CAA83264.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 121;
Best Local Similarity 73.3%; Pred. No. 3e-35;
Matches 85; Conservative 13; Mismatches 15; Indels 3; Gaps 2;

QY 2 BSGPGLVPAQTLSTLSCAVSGSIRSGYWSWIRHPGKGLWIGIYTHSGNTYNNPSL 61
DB 6 BSGPGLVKSPTSLTCTVSGYSSSYWMTROPKGKGLWIGIYTHSGNTYNNPSL 65

QY 62 KSRIMSVDTSENKSLRLNSVTAAADTAAYYCARLDG--YT-LDIMGQGLTVTSS 114
DB 66 KSRVITSDTKNSPGLKLSVTAADTAAYYCSRLSGGYSDPDYWSQGLTVTSS 121

RESULT 11

S31690
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31690
R/Ginsler, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31690
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-130 <CUI>
A/Cross-references: UNIPARC:UPI0000116471; EMBL:Z14199; NID:930984; PIDN:CAA78568.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/20-102/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 130;
Best Local Similarity 72.1%; Pred. No. 3.3e-35;
Matches 88; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 61
D 11 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 68
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112
D 69 KSRVTVSDTSKQPSLKSSTVADTAAYVYCARGSVLLMFGEILYFFYWGQGLTVTV 128

QY 113 SS 114
D 129 SS 130

RESULT 12

S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C/Accession: S19668; S24445
R/Markes, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A/Title: B γ -passing immunization. Human antibodies from V-gene libraries displayed on ph
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19668
A/Molecule type: mRNA
A/Residues: 1-127 <MAR>
A/Cross-references: UNIPARC:UPI0000176C7F; EMBL:X61648
R/Jones, P.T.
Submitted to the EMBL Data Library, October 1991
A/Reference number: S24442
A/Accession: S24445
A/Molecule type: mRNA
A/Residues: 1-118, 'E', '120-121', 'T', '123-126', 'F' <CON>
A/Cross-references: UNIPARC:UPI0000115FE7; EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 127;
Best Local Similarity 69.7%; Pred. No. 3.9e-35;
Matches 85; Conservative 15; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 61
D 6 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 65
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112
D 66 KSRVTVSDTSKQPSLKSSTVADTAAYVYCARGSVLLMFGEILYFFYWGQGLTVTV 125

QY 113 SS 114
D 126 SS 127

RESULT 13

S09711
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S09711
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A/Reference number: S09710; MUID:9026255; PMID:2111699
A/Accession: S09711
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-146 <HUG>
A/Cross-references: UNIPARC:UPI0000176CD3
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 146;
Best Local Similarity 68.0%; Pred. No. 4.6e-35;
Matches 83; Conservative 17; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 61
D 25 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 84
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112
D 85 KSRVTVSDTSKQPSLKSSTVADTAAYVYCARVLSRTSISQSYVMDVWGQGLTVTV 144

QY 113 SS 114
D 145 SS 146

RESULT 14

S31511
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31511
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A/Reference number: S31509
A/Accession: S31511
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-155 <CHA>
A/Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 449.5; DB 2; Length 155;
Best Local Similarity 70.8%; Pred. No. 6.1e-35;
Matches 85; Conservative 15; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 61
D 38 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 95
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 114
D 96 KSRVTVSDTSKQPSLKSSTVADTAAYVYCARGSVLLMFGEILYFFYWGQGLTVTV 155

RESULT 15

S31512

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S31512

R:Chaastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509

A:Accession: S31512

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CHA>

A:Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:933082; PIDN:CAA49494.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 446.5; DB 2; Length 155;

Best Local Similarity 70.0%; Pred. No. 1,2e-34;

Matches 84; Conservative 16; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGPGLVKPAQTLISCAVSGSIRSGYYWNIROHPGKLEWIGYIYHSGNTYYNPSL 61

DB 38 ESGPGLVKPSETLSLCTVSGSIS--YYWSWIRQPPGKLEWIGYIYTGSAATYNPPI 95

QY 62 KSRIMSVDTSEKKFSRLNSVTAADTAAYYCARLDG-----YTIIDIWGGTLVTYSS 114

DB 96 KSRVTISVDTSKNQFSLKVSSTVAADTAAYYCARGGGISWYVYTGMDVWGQGITVTYSS 155

Search completed: August 30, 2006, 00:42:55

Job time : 10.7091 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 62.1818 Seconds
(without alignments)
1695.862 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVPAQTLISLSCAV.....RLDGYTLIDMGQTLVTWSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483.5	79.4	476	2	Q6GMX1_HUMAN
2	473	77.7	478	2	Q7Z379_HUMAN
3	451	74.1	150	2	Q9S973_HUMAN
4	449	73.7	477	2	Q6GMX7_HUMAN
5	446.5	73.3	119	2	Q9UL73_HUMAN
6	444	72.9	465	2	Q6GMX6_HUMAN
7	440	72.2	576	2	Q6PA18_HUMAN
8	432	70.9	496	2	Q96KX8_HUMAN
9	430.5	70.7	492	2	Q7Z374_HUMAN
10	430	70.6	620	2	Q96EY0_HUMAN
11	419.5	68.9	129	1	HV2E_HUMAN
12	412.5	67.7	478	2	Q6NTH3_HUMAN
13	409.5	67.2	595	2	Q8WUX4_HUMAN
14	409.5	67.2	597	2	Q6GMX5_HUMAN
15	409.5	67.2	597	2	Q9BU10_HUMAN
16	409.5	67.2	625	2	Q96A46_HUMAN
17	408	67.0	139	2	Q86SX2_HUMAN
18	405.5	66.6	597	2	Q9BQB8_HUMAN
19	405	66.5	130	2	Q81ZD7_HUMAN
20	405	66.5	146	1	HV2I_HUMAN
21	389	63.9	483	2	Q5UAI3_MOUSE
22	388	63.7	473	2	Q8TC63_HUMAN
23	383	62.9	136	2	Q8LBO5_MOUSE
24	378.5	62.2	615	2	Q569B6_RAT
25	377.5	62.0	479	2	Q99M22_MOUSE
26	374.5	61.5	137	1	HV46_MOUSE
27	374	61.4	116	2	Q7Z3Y6_HUMAN
28	372.5	61.2	119	2	Q53VR3_HUMAN
29	370.5	60.8	115	2	Q53VQ1_MOUSE
30	370.5	60.8	262	2	Q65Z11_MOUSE
31	369.5	60.7	117	1	HV2G_HUMAN

32	366.5	60.2	590	2	Q569B8_RAT	Q569B8_rattus norv
33	364.5	59.9	119	2	Q53VQ5_MOUSE	Q53VQ5_mus musculus
34	362	59.4	120	2	Q53VR7_MOUSE	Q53VR7_mus musculus
35	362	59.4	122	2	Q9UL75_HUMAN	Q9UL75_homo sapien
36	361.5	59.4	113	1	HV47_MOUSE	P01823_mus musculus
37	357.5	58.7	476	2	Q6MZK7_HUMAN	Q6MZK7_homo sapien
38	353.5	58.0	119	2	Q53VR2_MOUSE	Q53VR2_mus musculus
39	352.5	57.9	98	2	Q53VR2_MOUSE	Q53VR2_mus musculus
40	349.5	57.4	477	2	Q510J1_RAT	Q510J1_rattus norv
41	342.5	56.2	116	1	HV61_MOUSE	P18532_mus musculus
42	341.5	56.1	116	1	HV61_MOUSE	P18531_mus musculus
43	338.5	55.6	98	2	Q53VQ4_MOUSE	Q53VQ4_mus musculus
44	334.5	54.9	98	2	Q53VQ8_MOUSE	Q53VQ8_mus musculus
45	334	54.8	117	1	HV62_MOUSE	P18533_mus musculus

ALIGNMENTS

RESULT 1
Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Shet N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira W.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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EMBL: BC073773; AAH73773.1; -; mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG-CL.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG-V.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; CL-set; 3.

DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KW SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 72.4%; Score 483.5; DB 2; Length 476;
 Best Local Similarity 72.4%; Pred. No. 7.1e-42;

Matches 90; Conservative 16; Mismatches 5; Indels 13; Gaps 2;

QY 2 ESGPGLVKEPAQTSLSCAVSGSIRSGYWSMIRQHPGKLEWIGYIHSGNTYVNSL 61
 DB 25 ESGPGLVKEPQTSLTCTVSGGSSISGDYWSMIRQHPGKLEWIGYIHSGNTYVNSL 84
 QY 62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCAR-----LDGYTLDIWGQTLV 110
 DB 85 KSRVTVISLDTSKNQFSLRNSVTADTAVYYFCARAGVGSFRSWALDGF--NIVGQGTWV 142
 QY 111 TVSS 114
 DB 143 TVSS 146

RESULT 2

072379_HUMAN

ID 072379_HUMAN PRELIMINARY; PRT; 478 AA.

AC 072379; Integrated into UniProtKB/TrEMBL.

DT 01-OCT-2003, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Hypothetical protein DKFZp686K04218 (Fragment).

GN Name=DKFZp686K04218.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Human rectum tumor;

RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amid C., Osanger A.,

Pofo G., Han M., Wiemann S.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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CC EMBL; BX538066; CAD97996.1; -; mRNA.

DR HSSP; P01820; 1G7J.

DR SMR; 072379; 248-456.

DR Ensembl; ENSG00000130076; Homo sapiens.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG_LIKE.

DR InterPro; IPR003597; IG_C1.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR InterPro; IPR013106; V-set.

DR Pfam; PF07654; C1-set; 2.

DR SMART; SM00409; IG; 1.

DR SMART; SM00407; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

DR Hypothetical protein; Immunoglobulin domain; Repeat.

FT NON TER 1

SEQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 77.7%; Score 473; DB 2; Length 478;
 Best Local Similarity 75.7%; Pred. No. 9e-41;
 Matches 87; Conservative 17; Mismatches 9; Indels 2; Gaps 1;

QY 2 ESGPGLVKEPAQTSLSCAVSGSIRSGYWSMIRQHPGKLEWIGYIHSGNTYVNSL 61
 DB 24 ESGPGLVKEPQTSLTCTVSGGSSISGDYWSMIRQHPGKLEWIGYIHSGNTYVNSL 83
 QY 62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARLDGY--TLDIWQGTLYVSS 114
 DB 84 KSRVTVISLDTSKNQFSLRNSVTADTAVYYFCARAGVGSFRSWALDGF--NIVGQGTWV 138

RESULT 3

095973_HUMAN

ID 095973_HUMAN PRELIMINARY; PRT; 150 AA.

AC 095973;

DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 1.

DT 07-FEB-2006, entry version 23.

DE VHA heavy chain variable region precursor (Fragment).

GN Name=IGM;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;

"Clonal proliferation of IGM secreting B cell in the synovium of

Behcet's patient with arthritis.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=92031262; PubMed=1718404;

RA Haridrarath N., Goldfarb I.S., Ikematsu H., Burastero S.E.;

Wilder R.L., Notkins A.L., Casali P.;

"Complete sequence of the genes encoding the VH and VL regions of low-

and high-affinity monoclonal IGM and IgA1 rheumatoid factors produced

by CD5+ B cells from a rheumatoid arthritis patient.";

Int. Immunol. 3:865-875(1991).

RL

CC

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CC

CC

CC EMBL; AF103795; AAC79084.1; -; mRNA.

DR PIR; S31673; S31673.

DR PIR; S78056; S78056.

DR HSSP; P01820; 1G7J.

DR SMR; 095973; 20-147.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG_LIKE.

DR InterPro; IPR003596; IG_V.

DR InterPro; IPR013106; V-set.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin domain; Signal.

FT SIGNAL 1 19

FT CHAIN 20 >150

FT NON TER 150

SEQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA1C9 CRC64;

Query Match 74.1%; Score 451; DB 2; Length 150;
 Best Local Similarity 74.3%; Pred. No. 5e-39;
 Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 2 ESGPGLVKEPAQTSLSCAVSGSIRSGYWSMIRQHPGKLEWIGYIHSGNTYVNSL 61
 DB 25 ESGPGLVKEPQTSLTCTVSGGSSISGDYWSMIRQHPGKLEWIGYIHSGNTYVNSL 84
 QY 62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARLDGYTLDIWGQTLTVSS 114
 DB 85 KSRVTVISLDTSKNQFSLRNSVTADTAVYYCARLGGAGDPFGHGHTVTVSS 137

RESULT 4
06GKX7_HUMAN PRELIMINARY; PRT; 477 AA.
ID 06GKX7_HUMAN
AC 06GKX7
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA DiCicco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshylnki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madden A., Rodriguez S., Sanchez A.,
RA Whiting M., Madden A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC
CC EMBL: BC073765; AAH73765.1; -, mRNA.
DR SRA; 06GKX7; 247-455.
DR Ensembl; ENSG00000150076; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IG1; 1.
DR SMART; SM00407; IG1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS50290; IG_MHC; UNKNOWN 2.
DR Hypothetical protein.
KW
SQ SEQUENCE 477 AA; 15631 MW; 9FE59C09C50CF85 CRC64;
Query Match 73.7%; Score 449; DB 2; Length 477;
Best Local Similarity 75.7%; Pred. No. 3e-36;
Matches 87; Conservative 10; Mismatches 14; Indels 4; Gaps 2;
2 ESFGPLVPAQTLISLSCAVSGSIRSGGYMSWIRQHGKGLWIGYIYHSGNTYNSPL 61
25 ESFGPLVPAQTLISLSCAVSGSIRSGGYMSWIRQHGKGLWIGYIYHSGNTYNSPL 82
62 KSRIAMVDISENKFSLRLNSVTADTAIVYICARIDG--YTLDIWGGQTLVTSS 114

Db 83 KSRRTLTSLDTSKNGFSLRLNSVTADTAVVYCAHGSSWDFAFDYGQGTTLVTSS 137

RESULT 5

O9UL73 HUMAN PRELIMINARY; PRT; 119 AA.

ID O9UL73 HUMAN

AC O9UL73

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 23.

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX NCBI

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=96277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;

RA Wu X., Lin B., Van der Werwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RT Clin. Immunol. Immunopathol. 87:184-192(1998).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=92078875; PubMed=160528; DOI=10.1084/jem.174.6.1639;

RA Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,

RA diamond B.;

RT "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype";

RT J. Exp. Med. 174:1639-1652(1991).

RL [3]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=90059975; PubMed=2511001;

RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;

RT "The smaller human VH gene families display remarkably little polymorphism";

RT EMO J. 8:3741-3748(1989).

RL -----

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CC -----

CC EMBL; AF035041; AAD56277.1; -; mRNA.

DR PIR; PH0876; PH0876.

DR PIR; S12416; S12416.

DR HSSP; P01820; 1G7J.

DR SMK; Q9UL73; 2-119.

DR LinkHub; Q9UL73; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig V.

DR InterPro; IPR013106; V-set.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin domain.

FT NON_TER 1

FT TER 1

FT SEQUENCE 119 AA; 13219 MW; 1BD866B6420EA0BE CRC64;

Query Match 73.3%; Score 446.5; DB 2; Length 119;

Best Local Similarity 74.1%; Pred. No. 1,1e-38;

Matches 86; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

QY 2 ESGFGLYKPAQTLSLSCAVSGGSGIRSGGIYWSWTRHHPGKLEWIGIYHSGNTYVNSL 61

DB 6 ESGGLYKPSSETLSITCTVSGSGSICS--YYSWTRHPPGKLEWIGIYHSGNTYVNSL 63

QY 62 KSRIRASVDTSNKFSLRLNSVTADTAVVYCAHLDG---YTLIHWGQGTTLVTYSS 114

DB 64 KSRRTLTSLDTSKNGFSLRLNSVTADTAVVYCAHLSWMPGPIYFPYWGQGTTLVTYSS 119

RESULT 6

ID	ORGANISM	PRELIMINARY:	PRT:	465 AA.
AC	O6GMX6_HUMAN			
AD	O6GMX6_HUMAN			
AE	O6GMX6_HUMAN			
AF	O6GMX6_HUMAN			
AG	O6GMX6_HUMAN			
AH	O6GMX6_HUMAN			
AI	O6GMX6_HUMAN			
AJ	O6GMX6_HUMAN			
AK	O6GMX6_HUMAN			
AL	O6GMX6_HUMAN			
AM	O6GMX6_HUMAN			
AN	O6GMX6_HUMAN			
AO	O6GMX6_HUMAN			
AP	O6GMX6_HUMAN			
AQ	O6GMX6_HUMAN			
AR	O6GMX6_HUMAN			
AS	O6GMX6_HUMAN			
AT	O6GMX6_HUMAN			
AV	O6GMX6_HUMAN			
AW	O6GMX6_HUMAN			
AX	O6GMX6_HUMAN			
AY	O6GMX6_HUMAN			
AZ	O6GMX6_HUMAN			
BA	O6GMX6_HUMAN			
BB	O6GMX6_HUMAN			
BC	O6GMX6_HUMAN			
BD	O6GMX6_HUMAN			
BE	O6GMX6_HUMAN			
BF	O6GMX6_HUMAN			
BG	O6GMX6_HUMAN			
BH	O6GMX6_HUMAN			
BI	O6GMX6_HUMAN			
BJ	O6GMX6_HUMAN			
BK	O6GMX6_HUMAN			
BL	O6GMX6_HUMAN			
BM	O6GMX6_HUMAN			
BN	O6GMX6_HUMAN			
BO	O6GMX6_HUMAN			
BP	O6GMX6_HUMAN			
BQ	O6GMX6_HUMAN			
BR	O6GMX6_HUMAN			
BS	O6GMX6_HUMAN			
BT	O6GMX6_HUMAN			
BV	O6GMX6_HUMAN			
BW	O6GMX6_HUMAN			
BX	O6GMX6_HUMAN			
BY	O6GMX6_HUMAN			
BZ	O6GMX6_HUMAN			
CA	O6GMX6_HUMAN			
CB	O6GMX6_HUMAN			
CC	O6GMX6_HUMAN			
CD	O6GMX6_HUMAN			
CE	O6GMX6_HUMAN			
CF	O6GMX6_HUMAN			
CG	O6GMX6_HUMAN			
CH	O6GMX6_HUMAN			
CI	O6GMX6_HUMAN			
CJ	O6GMX6_HUMAN			
CK	O6GMX6_HUMAN			
CL	O6GMX6_HUMAN			
CM	O6GMX6_HUMAN			
CN	O6GMX6_HUMAN			
CO	O6GMX6_HUMAN			
CP	O6GMX6_HUMAN			
CQ	O6GMX6_HUMAN			
CR	O6GMX6_HUMAN			
CS	O6GMX6_HUMAN			
CT	O6GMX6_HUMAN			
CU	O6GMX6_HUMAN			
CV	O6GMX6_HUMAN			
CW	O6GMX6_HUMAN			
CX	O6GMX6_HUMAN			
CY	O6GMX6_HUMAN			
CA	O6GMX6_HUMAN			
CB	O6GMX6_HUMAN			
CC	O6GMX6_HUMAN			
CD	O6GMX6_HUMAN			
CE	O6GMX6_HUMAN			
CF	O6GMX6_HUMAN			
CG	O6GMX6_HUMAN			
CH	O6GMX6_HUMAN			
CI	O6GMX6_HUMAN			
CJ	O6GMX6_HUMAN			
CK	O6GMX6_HUMAN			
CL	O6GMX6_HUMAN			
CM	O6GMX6_HUMAN			
CN	O6GMX6_HUMAN			
CO	O6GMX6_HUMAN			
CP	O6GMX6_HUMAN			
CQ	O6GMX6_HUMAN			
CR	O6GMX6_HUMAN			
CS	O6GMX6_HUMAN			
CT	O6GMX6_HUMAN			
CU	O6GMX6_HUMAN			
CV	O6GMX6_HUMAN			
CW	O6GMX6_HUMAN			
CX	O6GMX6_HUMAN			
CY	O6GMX6_HUMAN			
CA	O6GMX6_HUMAN			
CB	O6GMX6_HUMAN			
CC	O6GMX6_HUMAN			
CD	O6GMX6_HUMAN			
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CF	O6GMX6_HUMAN			
CG	O6GMX6_HUMAN			
CH	O6GMX6_HUMAN			
CI	O6GMX6_HUMAN			
CJ	O6GMX6_HUMAN			
CK	O6GMX6_HUMAN			
CL	O6GMX6_HUMAN			
CM	O6GMX6_HUMAN			
CN	O6GMX6_HUMAN			
CO	O6GMX6_HUMAN			
CP	O6GMX6_HUMAN			
CQ	O6GMX6_HUMAN			
CR	O6GMX6_HUMAN			
CS	O6GMX6_HUMAN			
CT	O6GMX6_HUMAN			
CU	O6GMX6_HUMAN			
CV	O6GMX6_HUMAN			
CW	O6GMX6_HUMAN			
CX	O6GMX6_HUMAN			
CY</				

[illegible]

01-DEC-2001, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 2.
07-FEB-2006, entry version 26.

IGM protein.

Name=IGHM;
GN Homo sapiens (Human) .
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
Homio.
NCBI_TaxID=9606;

[1]
NP NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
R Altschul S.F., Zeeberg B., Bluetow K.H., Schaefter C.F., Bat N.K.,
R Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R Ditschenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
R Stepien M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
R Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
R Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Halys S.W.,
R Villalón D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
R Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R Rodriguez A.R., Grimwood J., Schmutz J., Myers R.M.,
R Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
R Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
NP NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RG NIH MGC Project;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

[3]
NN NUCLEOTIDE SEQUENCE.
RP MEDLINE=91252286; PubMed=1904154;
RX Neale G.A., Kitchenman G.R.;
RA "mRNA transcripts initiating within the human immunoglobulin mu heavy
chain enhancer region contain a non-translatable exon and are
extremely heterogeneous at the 5' end."
RT Nucleic Acids Res. 19:2427-2433(1991).

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CC EMBL, BC011857, AAH11857.2; -; mRNA.
DR PIR, S15590; S15590.
DR HSSP, P01820; I67Y.
DR SMR, G96EXD; 27-251.
DR Ensembl, ENSG00000130076; Homo sapiens.
DR InterPro, IPR003599; IG.
DR InterPro, IPR007110; IG-1like.
DR InterPro, IPR003597; IG_C1.
DR InterPro, IPR003006; IG_MHC.
DR InterPro, IPR003596; IG_V.
DR InterPro, IPR013106; V-set.
DR Pfam, PF07654; C1-set; 4.
DR SMART, SM00409; IG_1.
DR SMART, SM00407; IGc1; 3.
DR PROSITE, PS50835; IG_LIKE; 5.
DR PROSITE, PS00290; IG_MHC; UNKOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A114A6E8FF27B CRC64;

Query Match 70.6%; Score 430; DB 2; Length 620;
Best Local Similarity 74.4%; Pred. No. 3; 9e-36;
Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2.

QY	2	ESGGGLVYKPAQGLTSLGAVSGGSIKSGGYWMSWRHQRPGKLEIGIYHSNGTYNPSL	61
Db	32	ESGGGLVYKPESTLTLVSGGSISS--YWSMIRDPAGKLEWIGIYHSNGTYNPSL	89
QY	62	KSRIAMSVDSISENKFSLRLNSVTADTAIVYYCA----RLDGYTLDIWGQGLTVVSS	114
Db	90	KSRIATMSVDISIKNGFSLKLSVTAADTAIVYYCASQPMELPTVGLFYWGQGLTVVSS	146
RESULT 11			
ID	HV2F_HUMAN	STANDARD;	PRT; 129 AA.
AC	P01824;		
DT	21-JUN-1986,	integrated into UniProtKB/Swiss-Prot.	
DT	21-JUL-1986,	sequence version 1.	
DT	07-MAR-2006,	entry version 36.	
DE	Ig heavy chain V-II region MAH.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
CC	NCBI_TaxID=9606;		
RN	[1]		
RP	PROTEIN SEQUENCE.		
RX	MEDLINE=82222235; PubMed=680618;		
RA	Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;		
RT	"Complete amino acid sequence of the delta heavy chain of human		
RL	immunoglobulin D.";		
CC	Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).		
CC	-I- MISCELLANEOUS: This chain was isolated from an IgD myeloma		
CC	protein.		
CC	-I- SIMILARITY: Contains 1 Ig-I like (immunoglobulin-like) domain.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-Nonetive License		
CC	-----		
DR	PIR; A02039; D2HWYA.		
DR	PDB; 1ZVO; X-ray; C/D=-.		
DR	SMR; P01824; 2-129.		
DR	GlycositeDB; P01824; --		
DR	GO; GO:0005576; C:extracellular region; NAS.		
DR	GO; GO:0003823; F:antigen binding; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-I like.		
DR	InterPro; IPR003596; IG V.		
DR	InterPro; IPR013106; V-sect.		
DR	Pfam; PF07686; V-sect; 1.		
DR	SMART; SM00409; IG; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG LIKE; 1.		
KM	3D-structure; Direct_protein sequencing; Immunoglobulin domain;		
KM	Immunoglobulin V region.		
FT	CHAIN 1		
FT	1 >129		
FT	Ig heavy chain V-II region MAH.		
FT	/FTid=PRO_0000059912.		
FT	IG-I like.		
FT	DOMAIN 1		
FT	NON TER 129		
FT	113		
FT	129		
FT	14117 MW; DSD5D347ABE51319 CRC64;		
FT	SQ SEQUENCE 129 AA;		
Query Match 68.9%; Score 419.5; DB 1; Length 129;			
Beet Local Similarity 62.7%; Pred. No. 8.6e-36;			
Matches 79; Conservative 16; Mismatches 16; Indels 15; Gaps 2.			
QY	2	ESGPGLVYKPAQGLTSLGAVSGGSIKSGGYWMSWRHQRPGKLEWIGIYHSNGTYNPSL	61
Db	6	ESGPGLVYKPESTLTLVSGGSISS--YWSMIRDPAGKLEWIGIYHSNGTYNPSL	65
QY	62	KSRIAMSVDSISENKFSLRLNSVTADTAIVYYCAR-----LDGYTLDIWGQGT	108
Db	66	KSRIVYISVDTSRNGSLNLKRSMSADTAIVYYCARGNPPYYDITGSGDDG-IDVWGQGT	123
QY	109	LVTYSS 114	

Db 124 TVHVS 129

RESULT 12

06NYH3_HUMAN PRELIMINARY; PRT; 478 AA.
 ID 06NYH3_HUMAN
 AC 06NYH3;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udén T.B., Toshyuk S., Carninci P., Prange C., Raha S.S., McMan P.J., McKernan K.J., Abramson R.D., Mullan S.J., Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC CopyRighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivative License
 CC EMBL: BC066594; AAH66594.1; -; mRNA.
 DR HSSP: P01820; 1A7N.
 DR SMR: Q6NTH3; 248-456.
 DR Ensemble: ENSG00000130076; Homo sapiens.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.
 DR Pfam: PF07654; C1-set; 2.
 DR SMART: SM00409; IG_1.
 DR SMART: SM00406; IG_2.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 478 AA; 51857 MW; 5FB898F60F07256 CRC64;

Query Match 67.7%; Score 412.5; DB 2; Length 478;

Best Local Similarity 66.9%; Pred. No. 2e-34; Matches 79; Conservative 17; Mismatches 13; Indels 9; Gaps 3;

Qy 2 ESGPGLVKPAQTLSTSCAVSGSIRSGGYWWSWIRQPGKGLWIGIYHSGNTYYPSTL 61

Db 25 ESGPGLVKPSEKTLSTLCVSIGDSINS--YVMSWIRKSPQCGMEWIGIYHSGNTYYPSTL 82

Qy 62 KSRIMSVTSEKRESLRINSTYADTANYICARLDG-----TLINOGTLYTVSS 114

Db 83 ESRVTSVDSIKDQFSKMLTSTYADTAITYCAR--GYGSKRYFDLWGVGVTVSS 138

RESULT 13

08WDX4_HUMAN PRELIMINARY; PRT; 595 AA.
 ID 08WDX4;
 AC 08WDX4;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2004, sequence version 2.
 DT 07-FEB-2006, entry version 24.
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udén T.B., Toshyuk S., Carninci P., Prange C., Raha S.S., McMan P.J., McKernan K.J., Abramson R.D., Mullan S.J., Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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 CC Distributed under the Creative Commons Attribution-NonDerivative License
 CC EMBL: BC019235; AAH19235.2; -; mRNA.
 DR HSSP: P01861; 1ADQ.
 DR SMR: Q8WDX4; 27-256.
 DR Ensemble: ENSG00000130076; Homo sapiens.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.

DR Pfam: PF07654; Cl-set; 4.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00407; IGC1; 3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IGMHC; UNKNOWN_3.
 DR Hypothetical protein.
 KW SEQUENCE 595 AA; 65291 MW; 0D4B50776545714E CRC64;
 Query March 67.2%; Score 409.5; DB 2: length 595;
 Match Local Similarity 66.7%; Pred. No. 5.3e-34;
 Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3
 Qy 4 GPGLVKPAQTLTSLSCAVSGSGSIRSGGYWMIROHPGKGLWIGYIHSGNTNPSLKS 63
 Db 34 GAGLLKPESETLSLTGCVGGSP--SGYVWSWIRQPGKGLWIGIHNSGNTNPSLKS 91
 Qy 64 RIMSVDPTSENKFSRLRNSVTRADTRAVTYCARL-----DG-YTLDWGGLTVTVSS 114
 Db 92 RVTISVDPSKQQLSLKSSVNAADTRAVYCARVITRASPGTDGRGMDVWGQGITVTVSS 151
 RESULT 14
 O6GMX5_HUMAN
 ID O6GMX5_HUMAN PRELIMINARY; PRT; 597 AA.
 AC O6GMX5;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE IGHM protein.
 GN Name=IGHM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lymph.
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,
 RA Klausner R. D., Collins F. S., Wagner L., Shennan C. M., Schuler G. D.,
 RA Altshul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
 RA Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,
 RA Stabileton M., Soares M. B., Bonaldi M. F., Casavant T. L., Scheetz T. E.,
 RA Brownstein M. J., Ushed T. B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,
 RA Bosak S. A., McEwan P. J., McKernan K. J., Malek J. A., Gunaratne P. H.,
 RA Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Huijck S. W.,
 RA Villalón D. K., Murzy D. M., Sodergren E. J., Lu X., Gibbs R. A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
 RA Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,
 RA Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M.,
 RA Bottingfield Y. S. N., Krzywinski M. I., Skalska U., Smalhus D. E.,
 RA Scherch A., Schein J. E., Jones S. J. M., Marra M. A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBD databases.
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 CC EMBL, BC073767; AAH73767.1; -; mRNA.
 DR SMR: O6GMX5: 20-249.
 DR Ensembl, ENSG00000130076; Homo sapiens.
 DR InterPro, IPR003599; IG.

Query Match	67.2%	Score 409.5	DB 2	Length 597
Best local Similarity	66.7%	Pred. No. 5.3e-34		
Matches 80	Conservative 14	Mismatches 15	Indels 11	Gaps 3
Qy	4	GPGLVKAQTLSTSCAVSGSIRSGCYWMSIROHPKGLIEWGIYHSGNTYNPSTLS	63	
Db	27	GAGLAKSETSLTLCGYGGSF--SGYVSWIRPPKGLIEWGEIHNHSGSTNYPSTLS	84	
Qy	64	RIAMSVDTSENKFSRLRNSTYAADTAVYVCARL-----DG-YTLIDWGQGLTVTVSS	114	
Db	85	RVTVISVDTSKKQSLSTKLSVVAADTAVYVCARVITRASPGDGRYGMVDVWGQGTITVTVSS	144	
RESULT 15				
Q9B010_HUMAN				
ID	Q9B010_HUMAN	PRELIMINARY	PRT	597 AA.
AC	Q9B010			
DT	01-JUN-2001	integrated into UniProtKB/TrEMBL.		
DT	01-JUN-2001	sequence version 1.		
DT	07-FEB-2006	entry version 27.		
DE	IGHM protein.			
GN	Name=IGHM;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homio.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NCILOTIDE SEQUENCE.			
RC	TISUE=Lymph;			
RC	MEBLIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshitsuki S., Catinini P., Prange C.,			
RA	Raba S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,			
RA	Schneher A., Schein J.E., Jones S.J.W., Maitra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RR	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NCILOTIDE SEQUENCE.			
RC	TISUE=Lymph;			
RG	NIH MGC Project;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
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; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;
; NUMBER OF SEQUENCES: 28
;
; CORRESPONDENCE ADDRESS:
;

```

```

ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREMITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PAMCTUT01
CLONE: 1513264
US-09-049-672A-4

Query Match: 81.9%; Score 499; DB 2; Length 473;
Best Local Similarity 78.2%; Pred. No. 5,8e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1

QY 2 ESGGVLVPAOTLSLSCAVSGGSIKRSGGYWSMIRQHGKGLKGLWIGIYHSGNTYYNPSL 61
Db 25 ESGGVLVPSSETLSLTCVSGGSIISGGIYMSWIRQPKGLKGLWIGIYHSGSTIYNPSL 84
QY 62 KSRIAMSVDTSENKESLRINSVTADTAIVYYCARLD-----GYTLDIWGQGLIVTVSS 114
Db 85 KSRVTVISDTSKNGSLKLSSTVADTAIVYYCARDDVGLRGNGYAMDVWGQGLIVTVSS 143

RESULT 3
US-09-472-087-7
Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OR INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPL
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      81.4% Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.5e-43;
Matches          91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

OY      3 SGPGLVPRACQTLSTSCAVSGGSIKRSIGGYWMSIRHPKGLEWIGIYHSGNTYYNPSLK 62
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1 SGPLVLVRSQLSLTCTVYSSGGSISSGGHYWSMIRHQHGKGLEWIGIYIGNTYNPNPSLK 60
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      63 SRIMSVDTSENKSKLRINSTAADPVTAVYYCARLDG--YTIDINGCGITLVYSS 114
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 SRVTISVTSKNQPSLKLKLSVTADPTAVYYCARDSDGYDGDVWGQGTTTVSS 114
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      81.4% Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.5e-43;
Matches          91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

OY      3 SGPGLVPRACQTLSTSCAVSGGSIKRSIGGYWMSIRHPKGLEWIGIYHSGNTYYNPSLK 62
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1 SGPLVLVRSQLSLTCTVYSSGGSISSGGHYWSMIRHPKGLEWIGIYIGNTYNPNPSLK 60
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      63 SRIMSVDTSENKSKLRINSTAADPVTAVYYCARLDG--YTIDINGCGITLVYSS 114
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 SRVTISVTSKNQPSLKLKLSVTADPTAVYYCARDSDGYDGDVWGQGTTTVSS 114
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
US-10-330-613A-25
; Sequence 25, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
APPLICANT: Gudae, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX 022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens

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US-10-330-613A-25

Query Match	81.2%	Score 494.5;	DB 2;	Length 119;
Best Local Similarity	82.6%	Pred. No. 3.2e-43;		
Matches 95; 'Conservative	8;	Mismatches 9;	Indels 3;	Gaps 2;

[illegible]

RESULT 6

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US-10-330-613A-5
Sequence 5, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABSENIX.022A
CURRENT APPLICATION NUMBER: US/10/330.613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 117
TYPE: RAT
ORGANISM: Homo Sapiens
US-10-330-613A-5

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Query Match	80.4%;	Score 489.5;	DB 2;	Length 117;
Best Local Similarity	81.6%;	Pred. No. 1e-42;		
Matches 93; Conservative	11;	Mismatches 7;	Indels 3;	Gaps 2;

[illegible]

RESULT 7

```

US-09-800-729-145
Sequence 145, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
  APPLICATION: Ni et al.
  TITLE OP INVENTION: 32 Human secreted proteins
  FILE REFERENCE: P204P1
  CURRENT APPLICATION NUMBER: US/09/800,729
  PRIOR FILING DATE: 2001-03-08
  PRIOR APPLICATION NUMBER: PCT/US00/26013
  PRIOR FILING DATE: 2000-09-22
  PRIOR APPLICATION NUMBER: 60/155,709
  PRIOR FILING DATE: 1999-09-24
  NUMBER OF SEQ ID NOS: 217
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 145
  LENGTH: 487
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-800-729-145

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Query Match	79.1%;	Score 482;	DB 2;	Length 487;
Best Local Similarity	74.8%;	Pred. No. 3.3e-41;		
Matches 92;	Conservative 12;	Mismatches 9;	Indels 10;	Gaps 2;

2 ESGPGLVPAQTLSLSCAVSGGIRSGGYWSWIRQHPGKLEWIGIYHSGNTYNNPSL 61

Db 25 ESGPGLVKPSETLSLCTVSGGSISSGHHYMSWIRQHPGKLEWIGYISYNGVTYYNPSL 84

62 KSR IAMSVDTS ENKFSLRLNSVTADTAVYYCAR-----LDGYTL-----DIWGQGLVT 11

Db 85 KSRVTISVDTSQÑQFSLRLSSVTADTAVYYCAKDHRA TRDGYQL EYRGFDYWGQILVT 14

QY	112	VSS	114
Db	145	VSS	147

RESULT 8

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US-10-330-613A-33
; Sequence 33, Application US/103030613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330.613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PR1
; ORGANISM: Homo Sapiens
US-10-330-613A-33

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Query Match	78.2%;	Score 476.5;	DB 2;	Length 117;
Best Local Similarity	78.9%;	Pred. No. 2.2e-41;		
Matches 90; Conservative	14;	Mismatches 7;	Indels 3;	Gaps 2

[illegible]

RESULT 9

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US-10-330-613A-37
Sequence 37, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENX1.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
PRIORITY DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ. ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 37
LENGTH: 121
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-37

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Query Match	77.6%	Score 472.5;	DB 2;	Length 121;
Best Local Similarity	76.3%	Pred. No. 5.9e-41;		
Matches	90;	Conservative 13;	Mismatches 8;	Indels 7;
				Gaps 2;
QY	2	ESGPGLYKPAQNTLSLCAVSGGSRSGGYWWSWIRHPRGKLEWIGYIYHSGNNYNNSTL	61	
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Db 6 ESGPGLVKPSETLSLCTVSGGSIST--YYWSMIRQPKGLBEMIGIYYTGNYYNPSL 63
QY 62 KSRIAMSVPTSEKFSRLNSVTAADTAAYYCA--DINGGTLVTVSS 114
Db 64 KSRVTVSDTSKQFSLKLSVTAADTAAYYCARDPQWLVPDAFDWGGTWSVSS 121

RESULT 10
US-08-360-125-5
Sequence 5, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURES:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best local Similarity 75.9%; Pred. No. 7.4e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTSLSCAVSGSIRSGYYWSMIRQPKGLBEMIGIYYTGNYYNPSL 61
Db 6 ESGPGLVKPSETLSLCTVSGGSISCGFYWMIRQPKGLBEMIGIYYSGSTYYNPSL 65
QY 62 KSRIAMSVPTSEKFSRLNSVTAADTAAYYCA--RLDGYTLDIWGGTLVTVSS 114
Db 66 KSRVTVSDTSKQFSLKLSVTAADTAAYYCARSTRLNG--ADYWGQGTMTVSS 119

RESULT 11
US-08-450-578-5
Sequence 5, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA: 07/905,534
APPLICATION NUMBER:
FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE:
ORGANELL:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.4e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGSIRSGYYWSWIRHPGKGLMIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSISGCFYWNIRHPGKGLMIGIYHSGNTYNNPSL 65

QY 62 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTYVSS 114
DB 66 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTYVSS 119

RESULT 12
US-09-017-628-5
Sequence 5, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:

APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Yoshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287ihiko
APPLICANT: NAGAIKE, Kazuhiro
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 119
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.4e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGSIRSGYYWSWIRHPGKGLMIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSISGCFYWNIRHPGKGLMIGIYHSGNTYNNPSL 65

QY 62 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTYVSS 114
DB 66 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTYVSS 119

RESULT 13
US-09-014-880-5
Sequence 5, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack, L.L.P.
STREET: 203 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.4e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTSLSCAVSGSIRSGYWSWIRHPGKGLWIGIYHSGNTYVNSL 61
Db 6 ESGPGLVKPSETSLTCTVSGSIS--YVMSWIRHPGKGLWIGIYHSGNTYVNSL 65

Qy 62 KSRIAMSVDTSENKFSRLNSVTADTAVYYCARLDG---YTLIDWGQTLVTYSS 114
Db 66 KSRVTISVDTSKQPSLKLSSVTADTAVYYCARSTLRG--ADYWGQGTMTYVSS 119

RESULT 14
US-09-025-769B-39
Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-025-769B-39

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 7.4e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTSLSCAVSGSIRSGYWSWIRHPGKGLWIGIYHSGNTYVNSL 61
Db 6 ESGPGLVKPSETSLTCTVSGSIS--YVMSWIRHPGKGLWIGIYHSGNTYVNSL 63

Qy 62 KSRIAMSVDTSENKFSRLNSVTADTAVYYCARLDG---YTLIDWGQTLVTYSS 114
Db 64 KSRVTISVDTSKQPSLKLSSVTADTAVYYCARWGDDGFYADYWGQGTMTYVSS 119

RESULT 15
US-09-025-769B-65
Sequence 65, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 7.4e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTSLSCAVSGSIRSGYWSWIRHPGKGLWIGIYHSGNTYVNSL 61
Db 6 ESGPGLVKPSETSLTCTVSGSIS--YVMSWIRHPGKGLWIGIYHSGNTYVNSL 63

Qy 62 KSRIAMSVDTSENKFSRLNSVTADTAVYYCARLDG---YTLIDWGQTLVTYSS 114
Db 64 KSRVTISVDTSKQPSLKLSSVTADTAVYYCARWGDDGFYADYWGQGTMTYVSS 119

Wed Aug 30 10:03:32 2006

Search completed: August 30, 2006, 00:37:11
Job time : 16.5455 secs

us-10-027-725a-7.ra1

Page 7

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 65.2909 Seconds
(without alignments)
808.788 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LBSGPELVKPAQTLISLSCAV.....RLDGYTLDIWGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	609	100.0	114	US-10-027-725A-7	Sequence 7, Appl1
2	556	91.3	114	US-10-027-725A-9	Sequence 9, Appl1
3	546	89.7	114	US-10-027-725A-8	Sequence 8, Appl1
4	519	85.2	122	US-10-309-762-147	Sequence 147, Appl1
5	518.5	85.1	121	US-10-309-762-152	Sequence 152, Appl1
6	517.5	85.0	125	US-10-309-762-11	Sequence 11, Appl1
7	514.5	84.5	121	US-10-309-762-151	Sequence 151, Appl1
8	512	84.1	118	US-10-309-762-138	Sequence 138, Appl1
9	512	84.1	120	US-10-309-762-13	Sequence 13, Appl1
10	512	84.1	120	US-10-309-762-144	Sequence 144, Appl1
11	509.5	83.7	123	US-10-309-762-12	Sequence 12, Appl1
12	509.5	83.7	123	US-10-309-762-13	Sequence 13, Appl1
13	509.5	83.7	123	US-10-309-762-14	Sequence 14, Appl1
14	508.5	83.5	123	US-10-309-762-10	Sequence 10, Appl1
15	508.5	83.5	123	US-10-309-762-18	Sequence 18, Appl1
16	508.5	83.5	123	US-10-309-762-19	Sequence 19, Appl1
17	508.5	83.5	125	US-10-309-762-8	Sequence 8, Appl1
18	508.5	83.5	125	US-10-309-762-16	Sequence 16, Appl1
19	508.5	83.5	144	US-10-893-576-35	Sequence 35, Appl1
20	506.5	83.2	119	US-10-309-762-131	Sequence 131, Appl1
21	505.5	83.0	119	US-10-309-762-140	Sequence 140, Appl1
22	505	82.9	252	US-09-880-748-1994	Sequence 1994, Appl1
23	505	82.9	252	US-10-293-418-1994	Sequence 1994, Appl1
24	505	82.9	252	US-11-054-515-1994	Sequence 1994, Appl1
25	505	82.9	252	US-11-266-444-1994	Sequence 1994, Appl1
26	504.5	82.8	125	US-10-309-762-153	Sequence 153, Appl1
27	504.5	82.8	480	US-10-910-901-6	Sequence 6, Appl1

28	504	82.8	120	US-10-309-762-139	Sequence 139, Appl1
29	503.5	82.7	127	US-10-309-762-14	Sequence 14, Appl1
30	503	82.6	124	US-10-309-762-75	Sequence 75, Appl1
31	503	82.6	143	US-10-309-762-96	Sequence 96, Appl1
32	501.5	82.3	117	US-10-330-613-13	Sequence 13, Appl1
33	501.5	82.3	117	US-10-330-530-13	Sequence 13, Appl1
34	501.5	82.3	117	US-10-660-357-13	Sequence 13, Appl1
35	501	82.3	149	US-10-910-901-22	Sequence 22, Appl1
36	500.5	82.2	123	US-10-893-576-190	Sequence 190, Appl1
37	500.5	82.2	251	US-10-120-414-75	Sequence 75, Appl1
38	500.5	82.2	251	US-10-992-195-75	Sequence 75, Appl1
39	500	82.1	125	US-10-805-177-53	Sequence 53, Appl1
40	498.5	81.9	253	US-09-880-748-1619	Sequence 1619, Appl1
41	498.5	81.9	253	US-10-293-418-1619	Sequence 1619, Appl1
42	498.5	81.9	253	US-11-054-515-1619	Sequence 1619, Appl1
43	498.5	81.9	253	US-11-266-444-1619	Sequence 1619, Appl1
44	497.5	81.7	148	US-10-893-576-31	Sequence 31, Appl1
45	497	81.6	110	US-10-309-762-74	Sequence 74, Appl1

ALIGNMENTS

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RESULT 1
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match      100.0%; Score 609; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.7e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LBSGPELVKPAQTLISLSCAVSGSIRSGYWSIRQHPKGLWIGYIHSGNTYVNS 60
      |||
DB      1 LBSGPELVKPAQTLISLSCAVSGSIRSGYWSIRQHPKGLWIGYIHSGNTYVNS 60
QY      61 LKSRIMSVDTSEKRSFLNSVTADTVVYCARLDGYTLDIWGQGLTVTVSS 114
      |||
DB      61 LKSRIMSVDTSEKRSFLNSVTADTVVYCARLDGYTLDIWGQGLTVTVSS 114

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
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Query Match	85.0%;	Score 517.5;	DB 4;	Length 125;
Best Local Similarity	81.7%;	Pred. No. 2.4e-40;		
Matches 98;	Conservative 9;	Mismatches 6;	Indels 7;	Gaps 2;

[illegible]

RESULT 7
US-10-309-762-151

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? Sequence 151, Application US/10309762
? Publication No. US20040018198A1
? GENERAL INFORMATION:
?
? APPLICANT: Gudas, Jean
? APPLICANT: Poltz, Ian
? APPLICANT: Handa, Masahisa
? APPLICANT: Gallo, Michael
? TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
? TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
? FILE REFERENCE: ABGENIX, 027A
? CURRENT APPLICATION NUMBER: US/10/309,762
? CURRENT FILING DATE: 2002-12-02
? PRIOR APPLICATION NUMBER: 60/337275
? PRIOR FILING DATE: 2001-12-03
? NUMBER OF SEQ ID NOS: 246
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 151
? LENGTH: 121
?
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-10-309-762-151

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Query Match	Score	DB	Length
84.5%	514.5	DB 4	Length 121;

Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;

Qy	2	ESGGGLVAKPQQTSLSLCAVSGGSGSIRSGGYWMSVIRHPGGLGLMIGIYHSGGTYNPNL	61
Db	6	ESGGGLVAKPQQTSLSLCTVSGGSGISSGGYWMSVIRHPGGLGLMIGIYHSGGTYNPNL	65
Qy	62	KSRILASVDTSENKFSRLNLSVTPADPAVYYCARL--DGYTIDINGGGTLYVSS	114
Db	66	KSRVTLTSDVTSKQPSLKLKLSVTPADPAVYYCARVLLMPEYGMDDWGQGTLYVSS	122

RESULT 8
US-10-309-762-138

; Sequence 138, Application US/10309762Z
; Publication No. US20040018198A1

APPLICANT: Gudas, Jean

APPLICANT: Handa, Masahisa

1. TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IN

FILE REFERENCE: ABGENIX.027A

CURRENT FILING DATE: 2002-12-02

PRIOR FILING DATE: 2001-12-03

; SOFTWARE: FastSeq for Windows Version 4.0.0

LENGTH: 118

ORGANISM: Homo sapiens

US-10-309-762-138

Query Match	84.1%;	Score 512;	DB 4;	Length 118;
Best Local Similarity	83.2%;	Pred. No. 7.2e-40;		
Matches 94;	Conservative 10;	Mismatches 9;	Indels 0;	Gaps 0;

Qy	Db
62	6
66	6
114	65
118	65

RESULT 9
US-10-309-762-13

```

Sequence 13. Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-13

```

Query Match	Score	DB	Length
84.1%	512	4	120

Matches	95;	Conservative	12;	Mismatches	5;	Indels	4;	Gaps	2;
---------	-----	--------------	-----	------------	----	--------	----	------	----

Qy 2 ESAGGLVKKPQPTLSLSCAVSGGSIIRSGGYXWMSVIRHPGKGLGEMIGYIYHSGNTVYNPBL 61
Db 6 ESEGGVLYKPSQTLSLTCVTSGGSSISSGGYXWMSVIRHPGKGLGEMIGYIYHSGNTVYNPBL 65
Qy 62 KSRIAMSVTSENNKPSRLNLSVTAAPTAVYVCARLDGYT---LDIWGGTGLTVVSS 114
Db 66 KSRITTSVDTSKNQFSLKLSSTVTAAPTAVYVCAR-DGYNWYFDMRGRTGLTVVSS 120

RESULT 10
US-10-309-762-144

; Sequence 144, Application US/10309762
; Publication No. US20040018198A1

APPLICANT: Gudas, Jear

APPLICANT: Handa, Masahisa

1. TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX

FILE REFERENCE: ABGENIX.0277

CURRENT FILING DATE: 2002-12-02

PRIOR FILING DATE: 2001-12-03

```
; SOFTWARE: FastSEQ for Windows Version 4.0
```

LENGTH: 120

```

; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      84.1%; Score 512; DB 4; Length 120;
Best Local Similarity 81.9%; Pred. No. 7.4e-40;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY      2  ESGGGLVKKPQTLSTLSCAVSGGSIIRSGGYWMTIRHKGKLEWIGYIYHSGNTYVPSL 61
DB      6  ESGGGLVKKPQTLSTLCTVSGGSIIRSGGYWMTIRHKGKLEWIGYIYHSGNTYVPSL 65

QY      62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARLDTG---LDIMQGTLVTYSS 114
DB      66 KSRIVTSVDTSKNQFSLKLSVTADTAVYYCAR-DGYNWYFDLWGRGLVTYSS 120

RESULT 11
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-12

Query Match      83.7%; Score 509.5; DB 4; Length 123;
Best Local Similarity 78.8%; Pred. No. 1.3e-39;
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

QY      2  ESGGGLVKKPQTLSTLSCAVSGGSIIRSGGYWMTIRHKGKLEWIGYIYHSGNTYVPSL 61
DB      6  ESGGGLVKKPQTLSTLCTVSGGSIIRSGGYWMTIRHKGKLEWIGYIYHSGNTYVPSL 65

QY      62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARL-----DGYTLDMQGTLVTYSS 114
DB      66 KSRIVTSVDTSKNQFSLKLSVTADTAVYYCAVLMFGEDYVDWVGCGTLVTYSS 123

RESULT 12
US-11-131-648-13
; Sequence 13, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
```

```

; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-13

Query Match      83.7%; Score 509.5; DB 6; Length 148;
Best Local Similarity 78.5%; Pred. No. 1.6e-39;
Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;

QY      2  ESGGGLVKKPQTLSTLSCAVSGGSIIRSGGYWMTIRHKGKLEWIGYIYHSGNTYVPSL 61
DB      15 ESGGGLVKKPQTLSTLCTVSGGSIIRSGGYWMTIRHKGKLEWIGYIYHSGNTYVPSL 74

QY      62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARLDTG-----YTLDMQGTLVTYSS 113
DB      75 KSRIVMSVDTSKNQFSLKLSVTADTAVYYCAR-DGIMINGYIGMDWVGCGTLVTYSS 133

QY      114 S 114
DB      134 S 134

RESULT 13
US-11-131-648-35
; Sequence 35, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-35

Query Match      83.7%; Score 509.5; DB 6; Length 148;
Best Local Similarity 78.5%; Pred. No. 1.6e-39;
```

Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYWMIROHPGKLEWIGYIHSGNTYNNPSL 61
Db 15 ESGPGLVKPQSTLSLCTVSGSSISGGYYWMIROHPGKLEWIGYIHSGNTYNNPSL 74
QY 62 KSRIANSVDTSENKFSRLNSVTADTAVYYCARLPG-----YTLDIWGQGLVTVSS 113
Db 75 KSRVITSVDTSENKQFSLKLSSTVTAADTAVYYCAR-DGIMIRGYYGMDVWGQGLVTVSS 133
QY 114 S 114
Db 134 S 134

RESULT 14

US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match 83.5%; Score 508.5; DB 4; Length 123;

Best Local Similarity 80.5%; Pred. No. 1.6e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYWMIROHPGKLEWIGYIHSGNTYNNPSL 61
Db 6 ESGPGLVKPQSTLSLCTVSGSSISGGYYWMIROHPGKLEWIGYIHSGNTYNNPSL 65
QY 62 KSRIANSVDTSENKFSRLNSVTADTAVYYCARLPG-----YTLDIWGQGLVTVSS 114
Db 66 KSRVITSVDTSENKQFSLKLSSTVTAADTAVYYCARAGKRYGSGSYLDVWGQGLVTVSS 123

RESULT 15

US-10-309-762-18
; Sequence 18, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-309-762-18

Query Match 83.5%; Score 508.5; DB 4; Length 123;

Best Local Similarity 80.5%; Pred. No. 1.6e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYWMIROHPGKLEWIGYIHSGNTYNNPSL 61
Db 6 ESGPGLVKPQSTLSLCTVSGSSISGGYYWMIROHPGKLEWIGYIHSGNTYNNPSL 65
QY 62 KSRIANSVDTSENKFSRLNSVTADTAVYYCARLPG-----YTLDIWGQGLVTVSS 114
Db 66 KSRVITSVDTSENKQFSLKLSSTVTAADTAVYYCARERVTDYGGYLDVWGQGLVTVSS 123

Search completed: August 30, 2006, 00:50:41
Job time: 66.2909 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 13.4727 Seconds
(without alignments)
578.960 Million cell updates/sec

Title: US-10-027-725a-7
Perfect score: 609
Sequence: 1 EESGPGLVKPAQTLISLSCAV.....RLDGYTLDIWGQTLVTVSS 114

Scoring table: BLOSUM62
Gapex 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications AA.New.*
1: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US09_NEW_PUB pep.*
2: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US06_NEW_PUB pep.*
3: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US07_NEW_PUB pep.*
4: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US08_NEW_PUB pep.*
5: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/PCT_NEW_PUB pep.*
6: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US10_NEW_PUB pep.*
7: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US11_NEW_PUB pep.*
8: /EMC_Celerra_SIDS3/Ptodata/2/pubppa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509.5	83.7	118	US-10-981-300-51	Sequence 51, App1
2	493.5	81.0	149	US-11-355-464-13	Sequence 13, App1
3	493.5	81.0	149	US-11-355-464-16	Sequence 16, App1
4	479.5	78.7	118	US-10-981-300-52	Sequence 52, App1
5	479.5	78.7	180	US-10-981-300-4	Sequence 4, App1
6	474	77.8	247	US-10-539-402-10	Sequence 10, App1
7	471.5	77.4	119	US-11-304-986-25	Sequence 25, App1
8	467.5	76.8	121	US-11-211-917-98	Sequence 98, App1
9	467.5	76.8	466	US-11-211-917-70	Sequence 70, App1
10	465.5	76.4	121	US-11-211-917-66	Sequence 66, App1
11	463	76.0	126	US-10-994-679-68	Sequence 68, App1
12	462.5	75.9	121	US-11-211-917-82	Sequence 82, App1
13	462.5	75.9	466	US-11-211-917-86	Sequence 86, App1
14	462	75.9	115	US-10-981-300-53	Sequence 53, App1
15	462	75.9	120	US-11-281-266-6	Sequence 6, App1
16	459.5	75.5	121	US-11-337-300-84	Sequence 84, App1
17	459.5	75.5	248	US-11-337-300-94	Sequence 94, App1
18	456	74.9	118	US-11-211-917-109	Sequence 109, App1
19	454	74.5	118	US-11-211-917-142	Sequence 142, App1
20	451.5	74.1	118	US-10-981-300-54	Sequence 54, App1
21	451.5	74.1	443	US-10-981-300-20	Sequence 20, App1
22	450	73.9	108	US-11-281-266-82	Sequence 82, App1
23	450	73.9	120	US-11-211-917-108	Sequence 108, App1
24	448.5	73.6	121	US-11-211-917-26	Sequence 26, App1
25	448.5	73.6	466	US-11-211-917-30	Sequence 30, App1

26	446.5	73.3	107	US-10-484-105-18	Sequence 18, App1
27	445.5	73.2	113	US-11-290-687-17	Sequence 17, App1
28	445	73.1	244	US-11-402-010-77	Sequence 77, App1
29	444.5	73.0	119	US-11-211-917-18	Sequence 18, App1
30	444.5	73.0	464	US-11-211-917-22	Sequence 22, App1
31	442.5	72.7	121	US-10-994-679-60	Sequence 60, App1
32	440	72.2	112	US-11-249-296-64	Sequence 64, App1
33	435	71.4	108	US-11-281-266-85	Sequence 85, App1
34	435	71.4	112	US-11-249-296-68	Sequence 68, App1
35	434	71.3	247	US-10-539-402-15	Sequence 15, App1
36	433	71.1	286	US-11-154-103-8	Sequence 8, App1
37	432	70.9	244	US-11-317-7868-17	Sequence 17, App1
38	432	70.9	448	US-11-317-7868-9	Sequence 9, App1
39	431	70.8	124	US-11-111-688-3	Sequence 3, App1
40	431	70.8	130	US-11-111-688-58	Sequence 58, App1
41	430.5	70.7	127	US-11-259-133-202	Sequence 202, App1
42	430	70.6	240	US-11-317-7868-15	Sequence 15, App1
43	430	70.6	445	US-11-317-7868-32	Sequence 32, App1
44	430	70.6	448	US-11-317-7868-7	Sequence 7, App1
45	429	70.4	124	US-11-111-688-1	Sequence 1, App1

ALIGNMENTS

RESULT 1
US-10-981-300-51
Sequence 51, Application US/10981300
Publication No. US2006009359A1
GENERAL INFORMATION:
APPLICANT: GIORGIO SENALDI
APPLICANT: GADI GAZIT-BORSTEIN
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
TITLE OF INVENTION: FOR MAKING AND USING THE SAME
FILE REFERENCE: ABGX-005
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-981-300-51

Query Match 83.7%; Score 509.5; DB 6; Length 118;
Best Local Similarity 83.2%; Pred. No. 1.1e-40;
Matches 94; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 2 EESGPGLVKPAQTLISLSCAVSGSIRSGYYWMIROHPGKLEWIGYIYHSGTYNPSL 61
DB 6 EESGPGLVKPSQTLISLCTVSGSGSYWMIROHPGKLEWIGYIYHSGTYNPSL 65
QY 62 KSRIVSVDSNKKQFSLKLSVTAADTAVYCARLDGYTLDIWGQTLVTVSS 114
DB 66 KSRVTVSDTSNKKQFSLKLSVTAADTAVYCARLDGYTLDIWGQTLVTVSS 117

RESULT 2
US-11-355-464-13
Sequence 13, Application US/11355464
Publication No. US20060147375A1
GENERAL INFORMATION:
APPLICANT: GUDAS, Sean
APPLICANT: JAKOBVITS, Aya
APPLICANT: JIA, Xiao-Chi,
APPLICANT: MORRISON, Robert Kendall,
APPLICANT: CHALILITA-EID, Pia M.
APPLICANT: RAITANO, Arthur B.
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
TITLE OF INVENTION: BIND TO PSCA PROTEINS
FILE REFERENCE: 511582008821
CURRENT APPLICATION NUMBER: US/11/355,464

```

; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US 11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-355-464-13
```

```

Query Match      81.0%; Score 493.5; DB 7; Length 149;
Best Local Similarity 76.9%; Pred. No. 4.2e-39;
Matches 93; Conservative 12; Mismatches 7; Indels 9; Gaps 2;
```

```

QY      2  ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 61
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4  ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 63
QY      62  KSRIVSVTSENKESLRLNSVTADTAAYYCARLDGYT-----LDIWGGTLVTVS 113
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64  KSRIVSVTSENKESLRLNSVTADTAAYYCAR-DHITWVRGVPKGMVWGGGTVTVS 122
QY      114 S 114
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      123 S 123
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 3
US-11-355-464-16
; Sequence 16, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: CHALILITA-ELID, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT APPLICATION NUMBER: US/11/355,464
; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US 11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
```

```

; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-355-464-16
```

```

Query Match      81.0%; Score 493.5; DB 7; Length 149;
Best Local Similarity 76.9%; Pred. No. 4.2e-39;
Matches 93; Conservative 12; Mismatches 7; Indels 9; Gaps 2;
```

```

QY      2  ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 61
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4  ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 63
QY      62  KSRIVSVTSENKESLRLNSVTADTAAYYCARLDGYT-----LDIWGGTLVTVS 113
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64  KSRIVSVTSENKESLRLNSVTADTAAYYCAR-DHITWVRGVPKGMVWGGGTVTVS 122
QY      114 S 114
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      123 S 123
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 4
US-10-981-300-52
; Sequence 52, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-981-300-52
```

```

Query Match      78.7%; Score 479.5; DB 6; Length 118;
Best Local Similarity 78.8%; Pred. No. 6.8e-38;
Matches 89; Conservative 11; Mismatches 12; Indels 1; Gaps 1;
```

```

QY      2  ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 61
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  QSGPGLVKPSQTLSTLCTVSGGSIIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 65
QY      62  KSRIVSVTSENKESLRLNSVTADTAAYYCARLDGYTLDIWGGTLVTVS 114
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRFTISVDSKQPSLKLTSVTADTAAYYCARLDGYT-FDYWGLGLTVTVSS 117
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 5
US-10-981-300-4
; Sequence 4, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: homo sapien
US-10-981-300-4
```

```
Query Match          78.7%; Score 479.5; DB 6; Length 180;
Best Local Similarity 78.8%; Pred. No. 1e-37;
Matches 89; Conservative 11; Mismatches 12; Indels 1; Gaps 1;
```

```
QY 2 ESGPGLVKAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 QSGPGLVKAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 65
```

```
QY 62 KSRIVSVPTSENKFSRLNLSVTAADTAVYYCARLDGTYLIDINGQGLTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRFTISVPTSKNPFSLKLTSTVTAADTAVYYCARLTDY-PDYWGLGLTVTVSS 117
```

```
RESULT 6
US-10-539-402-10
; Sequence 10, Application US/10539402
; Publication No. US20060115477A1
; GENERAL INFORMATION:
; APPLICANT: Xerion Pharmaceuticals AG
; APPLICANT: Tufts University
; TITLE OF INVENTION: Neuropilin-1 Inhibitor
; FILE REFERENCE: XE12BPC
; CURRENT APPLICATION NUMBER: US/10/539,402
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 60/435,893
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: EP 03000615
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-10-539-402-10
```

```
Query Match          77.8%; Score 474; DB 6; Length 247;
Best Local Similarity 75.7%; Pred. No. 4.6e-37;
Matches 87; Conservative 16; Mismatches 6; Indels 6; Gaps 2;
```

```
QY 4 GPELVKPAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 GPELVKASETILSINCTVSGSSLSGGYWMIRQHPGKGLWIGIYHSGNTYNNPSL 68
QY 64 RIMSVDTSENKFSRLNLSVTAADTAVYYCARL---DGYTLIDINGQGLTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 RVTISVPTSKNPFSLKLTSTVTAADTAVYYCARVPLRDFG--DVMGGGLTVTVSS 121
```

```
RESULT 7
US-11-304-986-25
; Sequence 25, Application US/11304986
; Publication No. US20060165682A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth and NeutraLab et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; FILE REFERENCE: ELN-055
; CURRENT APPLICATION NUMBER: US/11/304,986
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: 60/636684
; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct, consensus sequence for heavy chain
; OTHER INFORMATION: framework region
US-11-304-986-25
```

```
Query Match          77.4%; Score 471.5; DB 7; Length 119;
Best Local Similarity 77.6%; Pred. No. 3.8e-37;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;
```

```
QY 2 ESGPGLVKAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 63
```

```
QY 62 KSRIVSVPTSENKFSRLNLSVTAADTAVYYCARLDG---YTLIDINGQGLTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTSVPTSKNPFSLKLTSTVTAADTAVYYCARWGSDGGRYANDYWGQGLTVTVSS 119
```

```
RESULT 8
US-11-211-917-98
; Sequence 98, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-98
```

```
Query Match          76.8%; Score 467.5; DB 7; Length 121;
Best Local Similarity 77.1%; Pred. No. 9.2e-37;
Matches 91; Conservative 10; Mismatches 10; Indels 7; Gaps 2;
```

```
QY 2 ESGPGLVKAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKAQTLISCAVSGGSIIRSGGYWMIROHPGKGLWIGIYHSGNTYNNPSL 63
QY 62 KSRIVSVPTSENKFSRLNLSVTAADTAVYYCARLDGTYLID---WGQGLTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTSVPTSKNPFSLKLTSTVTAADTAVYYCARKGLVGDYGMFAPWGQGLTVTVSS 121
```

```
RESULT 9
US-11-211-917-70
; Sequence 70, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
```

;; PRIOR FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 60/348,980
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 70
;; LENGTH: 466
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-211-917-70

Query Match 76.8%; Score 467.5; DB 7; Length 466;
Best Local Similarity 77.1%; Pred. No. 3.5e-36;
Matches 91; Conservative 10; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESEBGLVKPAQTLISCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 61
DB 25 ESEBGLVKPSELTSLCTVSGGSIR--GYWSWIRPDPGKLEWIGIYHSNTYNSPL 82
QY 62 KSRIVSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 114
DB 83 KSRIVSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 140

RESULT 10
US-11-211-917-66
;; Sequence 66; Application US/11211917
;; Publication No. US2006093600A1
;; GENERAL INFORMATION:
;; APPLICANT: BEDIAN, VAHE
;; APPLICANT: GLADUE, RONALD P.
;; APPLICANT: CORVALAN, JOSE
;; APPLICANT: JIA, XIAO-CHI.
;; APPLICANT: PENG, XIAO
;; TITLE OF INVENTION: ANTIBODIES TO CD40
;; FILE REFERENCE: ABX-PF/3 US
;; CURRENT APPLICATION NUMBER: US/11/211,917
;; CURRENT FILING DATE: 2005-08-25
;; PRIOR APPLICATION NUMBER: US/10/292,088
;; PRIOR FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 60/348,980
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 66
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-211-917-66

Query Match 76.4%; Score 465.5; DB 7; Length 121;
Best Local Similarity 77.1%; Pred. No. 1.4e-36;
Matches 91; Conservative 9; Mismatches 11; Indels 7; Gaps 2;

QY 2 ESEBGLVKPAQTLISCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 61
DB 6 ESEBGLVKPSELTSLCTVSGGSIR--GYWSWIRPDPGKLEWIGIYHSNTYNSPL 63
QY 62 KSRIVSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 114
DB 64 KSRIVSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 121

RESULT 11
US-10-994-679-68
;; Sequence 68; Application US/10994679
;; Publication No. US2006011559A2
;; GENERAL INFORMATION:
;; APPLICANT: ROSEN, CRAIG A.
;; APPLICANT: ROSEN, CRAIG A.
;; APPLICANT: RUBEN, STEVEN M.
;; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;; FILE REFERENCE: 1488.1150001

;; CURRENT APPLICATION NUMBER: US/10/994,679
;; CURRENT FILING DATE: 2004-11-23
;; PRIOR APPLICATION NUMBER: US/10/067,800
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: PCT/US01/04153
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 09/779,880
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/297,257
;; PRIOR FILING DATE: 2001-06-12
;; PRIOR APPLICATION NUMBER: 60/310,458
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: 60/328,447
;; PRIOR FILING DATE: 2001-10-12
;; PRIOR APPLICATION NUMBER: 60/341,725
;; PRIOR FILING DATE: 2001-12-21
;; NUMBER OF SEQ ID NOS: 70
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 126
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-994-679-68

Query Match 76.0%; Score 463; DB 6; Length 126;
Best Local Similarity 72.6%; Pred. No. 2.5e-36;
Matches 90; Conservative 15; Mismatches 7; Indels 12; Gaps 3;

QY 1 ESEBGLVKPAQTLISCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 60
DB 5 ESEBGLVKPSELTSLCTVSGGSIR--GYWSWIRPDPGKLEWIGIYHSNTYNSPL 62
QY 61 KSRIVSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 110
DB 63 KSRIVSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 122
QY 111 TVSS 114
DB 123 TVSS 126

RESULT 12
US-11-211-917-82
;; Sequence 82; Application US/11211917
;; Publication No. US2006093600A1
;; GENERAL INFORMATION:
;; APPLICANT: BEDIAN, VAHE
;; APPLICANT: GLADUE, RONALD P.
;; APPLICANT: CORVALAN, JOSE
;; APPLICANT: JIA, XIAO-CHI
;; APPLICANT: PENG, XIAO
;; TITLE OF INVENTION: ANTIBODIES TO CD40
;; FILE REFERENCE: ABX-PF/3 US
;; CURRENT APPLICATION NUMBER: US/11/211,917
;; CURRENT FILING DATE: 2005-08-25
;; PRIOR APPLICATION NUMBER: US/10/292,088
;; PRIOR FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 60/348,980
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 82
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-211-917-82

Query Match 75.9%; Score 462.5; DB 7; Length 121;
Best Local Similarity 76.3%; Pred. No. 2.7e-36;
Matches 90; Conservative 11; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESEBGLVKPAQTLISCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 61
DB 25 ESEBGLVKPSELTSLCTVSGGSIR--GYWSWIRPDPGKLEWIGIYHSNTYNSPL 82

Db 6 ESSEGLVKPSETSLTCTVAGGSR--GYTMSINRQPGKGLMIGITIISSSTNNPSL 63

Qy 62 KSRIAMVDPSSENKESRLINSVTAADTAAYVYCARLQGYTLDI-----WGQGLVTYSS 114

Db 64 KSRITIVSDTSKIQFSLKSSVTAADTAAYVYCARRGLGYDYDYGMAPWGQGLVTYSS 121

```

RESULT 13
US-11-211-917-86
Sequence 86, Application US/11/211917
Publication NO. US20060093600A1
GENERAL INFORMATION:
APPLICANT: BEDINI, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: PENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR APPLICATION NUMBER: US/10/292,088
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 466
TYPE: PRT
ORGANISM: Homo sapiens
US-11-211-917-86

```

Query Match	75.9%	Score 462.5	DB 7	Length 466
Best Local Similarity	76.3%	Pred No. 1e-35		
Matches 90	Conservative 11	Mismatches 10	Indels 7	Gaps 2

Qy 2 ESAGGLVMPADLTLSLCAVSCGSLRSGGYWMTLRHPGKGLKELIGYIYSSGNTYNNPSL 6
Db 25 ESAGGLVMPSTLTSLCTVSCGSLR--GYWMTLRQPGKGLKELIGYIYSSGNTNNPSL 8
Qy 62 KSRITAMSVDTSENKFSRLNLSVTADPAVYTCARLDGYTLDT-----WGCTLVYVSS 114
Db 83 KSRITITSDTSKNQFSLTLSSVTADPAVYTCARGLGYDGMFAPMGQSTLVVSS 140

```

RESULT 14
US-10-981-300-53
: Sequence 53, Application US/10981300
: Publication NO. US2006009359A1
: GENERAL INFORMATION:
: APPLICANT: GIORGIO SENALDI
: TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODY
: TITLE OF INVENTION: FOR MAKING AND USING
: FILE REFERENCE: ABG-005
: CURRENT APPLICATION NUMBER: US/10/981,300
: CURRENT FILING DATE: 2004-11-03
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: FastSeq for Windows Version 4.0.0
: SEQ ID NO 53
: LENGTH: 115
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-981-300-53

```

Query Match	75.9%	Score 462;	DB: 6;	Length 115;
Best Local Similarity	77.9%	Pred: No. 2.8e-36;		
Matches 88; Conservative	12;	Mismatches 9;	Indels 4;	Gaps 2

Oy 2 ESGPGLVKPAQTSLSCAVSGGSIRGGYYWMIQHPPGKLEWIGIYIHSGNTTYNP SL 61
|||::|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 6 ESGPGLVKPSETSLTCTVSSGGSIS--YWSMWIQPPGKLEWIGIYIYSGSTNNYP SL 67

```

QY      62 KSRAMSVDTSENKFSRLNSVTADTAVYYCARLDDGYTLIDIMGGGLTVTSS 114
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      64 KSRRTISVDTSKNQFSRLKLSVTADTAVYYCAW--NYAFDIMGGGIMTVTSS 114

```

```

RESULT 15
US-11-281-266-6
; Sequence 6, Application US/11281266
; Publication No. US20060140948A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Paggioli, Raffaella
; APPLICANT: Senaldi, Giorgio
; APPLICANT: Manchlenko, Katly
; APPLICANT: Kang, Jaespal
; APPLICANT: Rathnaswami, Palaniswami
; APPLICANT: Ahluwalia, Ktiwan
; APPLICANT: Poord, Orit
; APPLICANT: Kikand, Scott
; TITLE OF INVENTION: FULLY HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: IL-13
; FILE REFERENCE: ABGENIX.119A
; CURRENT APPLICATION NUMBER: US/11/281, 266
; CURRENT FILING DATE: 2005-11-16
; PRIOR APPLICATION NUMBER: 60/629, 135
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: 60/728, 604
; PRIOR FILING DATE: 2005-10-19
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-281-266-6

```

Query Match	75.9%	Score 462	DB 7	Length 120
Best Local Similarity	75.2%	Pred. No. 3e-36		
Matches 88	Conservative 14	Mismatches 9	Indels 6	Gaps 2

QY 2 EESGGLVKKPQQTLSLSCAVSGGSIIRSGCGYWSMIRHPGKGLMIGIYHSGTATYNSPL 6

Db 6 EESGGLVKKPSETLSLCTVSGGSIIST--YMSMIRQPGKGLMIGIYVSGSTNNPSL 6

QY 62 KSRIRAMVDHSEKKESRLMSVTAPPAATPAVYVCARLDGY----TLIDMGOSTIVTYS 114

Db 64 KSRITIVDSIKQDFSLKLSVTPADPAVYVCARDGHTYDDAFIDMGOSTIVTYS 120

Search completed: August 30, 2006, 00:52:04
Job time : 14.4727 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 / Search time 102.427 Seconds
(without alignments)
508.875 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LBSGPGVLRPSQTLSTLCTV.....RSDPYTLDMWGQGLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	605	98.5	114	5	ABG30447 Human IGE
2	600	97.7	114	5	ABG30446 Human IGE
3	586	90.6	114	5	ABG30445 Human IGE
4	532.5	86.7	121	10	Aef11064 High freq
5	524.5	85.4	121	7	ADP03982 Murine-ex
6	524	85.3	118	7	ADP03968 Murine-ex
7	523.5	85.3	123	7	ADP03870 Murine-ex
8	521	84.9	120	7	ADP03974 Murine-ex
9	521	84.9	120	7	ADP03873 Murine-ex
10	521	84.9	122	7	ADP03977 Murine-ex
11	521	84.9	473	4	AAB36206 Human imm
12	520	84.7	221	7	ADJ32126 Human int
13	519.5	84.6	121	7	ADP03981 Murine-ex
14	519.5	84.6	125	7	ADP03871 Murine-ex
15	517.5	84.3	119	7	ADP03970 Murine-ex
16	517.5	84.3	148	10	AEB94855 Antibody
17	517.5	84.3	148	10	AEB94853 Antibody
18	516.5	84.1	123	2	AAW78433 Antibody
19	516.5	84.1	123	5	ABB97976 Heavy cha
20	516.5	84.1	123	7	ADG88414 Anti-Ob-R
21	516.5	84.1	123	7	ADP03872 Murine-ex
22	516.5	84.1	144	9	ADX98263 Human ant
23	516	84.0	124	7	ADP03935 Murine-ex

ALIGNMENTS

24	515.5	84.0	117	7	ADC99784	Adc99784 Anti-huma
25	515.5	84.0	117	7	ADDO5388	AdDO5388 Anti-MUC1
26	515.5	84.0	117	7	ADF09826	Adf09826 Human ant
27	515.5	83.9	125	8	ADs16556	Ads16556 Human ant
28	514	83.7	120	7	ADP03958	Adp03958 Murine-ex
29	514	83.7	120	7	ADP03969	Adp03969 Murine-ex
30	514	83.7	121	7	ADJ80377	Adj80377 Antibody
31	514	83.7	121	8	ADs16559	Ads16559 Human ant
32	514	83.7	122	9	AEA21492	Aea21492 Human ant
33	513.5	83.6	120	4	AAB62775	Aab62775 Human HIV
34	513	83.6	116	7	ADP03957	Adp03957 Murine-ex
35	512.5	83.5	125	7	ADP03868	Adp03868 Murine-ex
36	512.5	83.5	125	7	ADP03876	Adp03876 Murine-ex
37	512.5	83.5	480	9	ADZ57697	Adz57697 Anti-CMet
38	512	83.4	123	4	AA862745	Aab62745 Human HIV
39	511.5	83.3	119	7	ADP03961	Adp03961 Murine-ex
40	511.5	83.3	140	9	ADX98269	Adx98269 Human ant
41	511	83.2	110	7	ADP03934	Adp03934 Murine-ex
42	510.5	83.1	122	4	AAB62765	Aab62765 Human HIV
43	510.5	83.1	123	7	ADP03869	Adp03869 Murine-ex
44	510.5	83.1	127	7	ADP03874	Adp03874 Murine-ex
45	510.5	83.1	148	9	ADX98259	Adx98259 Human ant

RESULT 1	ABG30447	standard; protein; 114 AA.
ID	ABG30447	
XX	ABG30447;	
AC	21-OCT-2002	(first entry)
XX		
DT	21-OCT-2002	(first entry)
XX		
DE	Human IGE Fab clone 100 heavy chain protein.	
XX		
KW	Human; fab; anti-allergic; vaccine; grass pollen; Phl p 2;	
KM	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..26
FT		/note="FR1 region"
FT	Region	27..33
FT		/note="CDR1 region"
FT	Region	34..47
FT		/note="FR2 region"
FT	Region	48..63
FT		/note="CDR2 protein"
FT	Region	64..95
FT		/note="FR3 region"
FT	Region	96..103
FT		/note="CDR2 region"
FT	Region	104..114
FT		/note="FR4 region"
XX		
WO	WO200253595-A1.	
XX		
PD	11-JUL-2002.	
XX		
XX	27-DEC-2001, 2001WO-SR002908.	
PF	29-DEC-2000, 2000SE-00004892.	
PR		
XX		
PA	(PHAA) PHARMACIA DIAGNOSTICS AB.	
XX		
PI	Flicker'S, Steinberger P, Kraft D, Valenta R;	
XX	WPI, 2002-583604/62.	
DR	N-PSDB; ABR9639.	
XX		

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.
 XX
 XX
 PS Disclosure; Page 38; 45pp; English.
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific Fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The Fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific Fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
 CC Fab, clone 100 heavy chain protein of the invention
 CC
 XX Sequence 114 AA;
 SQ
 Query Match 98.5%; Score 605; DB 5; Length 114;
 Best Local Similarity 99.1%; Pred. No. 4,1e-44;
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSNTYVNS 60
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSNTYVNS 60
 QY 61 LKSRVTMSVDTSKNHSRLTSVTADTAAYVYCARSDGYTLDMWGQGLTVTVSS 114
 DB 61 LKSRVTMSVDTSKNHSRLTSVTADTAAYVYCARSDGYTLDMWGQGLTVTVSS 114
 RESULT 2
 ABG30446
 ID ABG30446 standard; protein; 114 AA.
 AC ABG30446;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Human IgE Fab clone 60 heavy chain protein.
 DE
 XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
 KM timothy grass pollen allergen; passive immunotherapy.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Location/Qualifiers
 FH 1..26
 FT /note= "FR1 region"
 FT 27..33
 FT /note= "CDR1 region"
 FT 34..47
 FT /note= "FR2 region"
 FT 48..63
 FT /note= "CDR2 protein"
 FT 64..95
 FT /note= "FR3 region"
 FT 96..103
 FT /note= "CDR2 region"
 FT 104..114
 FT /note= "FR4 region"
 FT
 XX WO200253595-A1.
 XX
 PD 11-JUL-2002.
 XX

PF 27-DEC-2001; 2001WO-SE002908.
 XX
 XX 29-DEC-2000; 2000SE-00004892.
 XX
 XX (PHAA) PHARMACIA DIAGNOSTICS AB.
 XX
 XX Flicker S, Steinberger P, Kraft D, Valenta R;
 XX
 DR WPI; 2002-563604/62.
 DR N-PSDB; ABK9638.
 XX
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.
 XX
 XX
 PS Disclosure; Page 37; 45pp; English.
 XX
 XX
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific Fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The Fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific Fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
 CC Fab, clone 60 heavy chain protein of the invention
 CC
 XX Sequence 114 AA;
 SQ
 Query Match 97.7%; Score 600; DB 5; Length 114;
 Best Local Similarity 96.5%; Pred. No. 1,1e-43;
 Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSNTYVNS 60
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSNTYVNS 60
 QY 61 LKSRVTMSVDTSKNHSRLTSVTADTAAYVYCARSDGYTLDMWGQGLTVTVSS 114
 DB 61 LKSRVTMSVDTSKNHSRLTSVTADTAAYVYCARSDGYTLDMWGQGLTVTVSS 114
 RESULT 3
 ABG30445
 ID ABG30445 standard; protein; 114 AA.
 AC ABG30445;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Human IgE Fab clone 94 heavy chain protein.
 DE
 XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
 KM timothy grass pollen allergen; passive immunotherapy.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Location/Qualifiers
 FH 1..26
 FT /note= "FR1 region"
 FT 27..33
 FT /note= "CDR1 region"
 FT 34..47
 FT /note= "FR2 region"
 FT 48..63
 FT /note= "CDR2 protein"
 FT
 XX


```

ADP03982
ID ADP03982 standard; protein; 121 AA.
XX
AC ADP03982;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytosolic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudae J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 152; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytosolic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
SQ Sequence 121 AA;
XX
Query Match 85.4%; Score 524.5; DB 7; Length 121;
Best Local Similarity 86.2%; Pred. No. 3.3e-37;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
XX
QY 2 EESGGLVPSQTLSTCTVSGSGSIRSGYWSWIRPGKLEWIGYIYHSGNTYNPSTL 61
DB 6 EESGGLVPSQTLSTCTVSGSGSIRSGYWSWIRPGKLEWIGYIYHSGNTYNPSTL 65
XX
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSD--GYTLDMNGGTLVTWSS 114
DB 66 KSRVTISVDTSKNQFSLRLSSVTADTAVYYCAYYDILDTGAFDLMGGTMTWTVSS 121
XX
RESULT 6
ADP03968
ID ADP03968 standard; protein; 118 AA.
XX
AC ADP03968;
XX
DT 29-JUL-2004 (first entry)

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XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytosolic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudae J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 138; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytosolic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
SQ Sequence 118 AA;
XX
Query Match 85.3%; Score 524; DB 7; Length 118;
Best Local Similarity 88.5%; Pred. No. 3.6e-37;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
XX
QY 2 EESGGLVPSQTLSTCTVSGSGSIRSGYWSWIRPGKLEWIGYIYHSGNTYNPSTL 61
DB 6 EESGGLVPSQTLSTCTVSGSGSIRSGYWSWIRPGKLEWIGYIYHSGNTYNPSTL 65
XX
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGGTLVTWSS 114
DB 66 KSRVTISVDTSKNQFSLRLSSVTADTAVYYCARYYGSDDYVGGTGLVTWSS 118
XX
RESULT 7
ADP03870
ID ADP03870 standard; protein; 123 AA.
XX
AC ADP03870;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytosolic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;

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	OS	Unidentified.
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;	
KW	gene therapy; murine; mouse; human; heavy chain variable domain.	
XX		
XX		
PN	WO2003048328-A2.	
XX		
PD	12-JUN-2003.	
PF	02-DEC-2002; 2002WO-US038550.	
PR	03-DEC-2001; 2001US-0337275P.	
PA	(ABGE-) ABGENIX INC.	
PI	Gudas J, Foltz I, Handa M, Gallo M,	
PI	WPI; 2003-523295/49.	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,	
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical	
PS	intraepithelial squamous and glandular neoplasia or esophageal tumors.	
XX		
XX	Claim 1; SEQ ID NO 10; 89pp; English.	
CC	The invention relates to a novel isolated monoclonal antibody (mAb)	
CC	comprising a heavy chain polypeptide and light chain polypeptide having a	
CC	sequence chosen from one of 53 fully defined amino acid sequences given	
CC	in the specification, where the antibody specifically binds carbonic	
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention	
CC	demonstrates cytostatic activity and may be useful for treating a tumour,	
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,	
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal	
CC	tumour or breast cancer, possibly via gene therapy. The current sequence	
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH	
CC	(heavy chain variable domain) protein of the invention. The protein was	
CC	generated via the introduction of the human CA IX protein into a	
CC	transgenic mouse strain.	
XX		
SQ	Sequence 123 AA;	
	Query March 85.3%; Score 523.5; DB 7; Length 123;	
	Best Local Similarity 85.6%; Pred. No. 4,1e-37;	
	Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1	
OY	2 ESGGGLVSPQTLSTCTVGSGSIRGGYMSWIROPKGLEMIIGIYHSGNTYYNPSL 61	
DB	6 ESGGGLVSPQTLSTCTVGSGSISGGYMSWIHQHFKGLEMIIGIYHSSTYYNSL 65	
OY	62 KSRVTMSVDTSKNHESLRLSVTAADTAVVYCARS-----DGYTLNNQGGLTVTSS 114	
DB	66 KSRVTIVSDTSKNQSLKLSSSVTAADTAVVYCARAGKYTGSGSYLDYWGQGLTVTVSS 123	
RESULT 8		
ID	ADP03974 standard; protein; 120 AA.	
AC	ADP03974;	
XX		
DT	29-JUL-2004 (first entry)	
XX		
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.	
XX		
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;	
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;	
KM	cervical intraepithelial squamous neoplasia;	
KW	gene therapy; murine; mouse; human; heavy chain variable domain.	
XX		
OS	Unidentified.	
PN	WO2003048328-A2.	

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PD PD      12-JUN-2003.
XX PF      02-DEC-2002; 2002WKO-USO38550.
XX PF      03-DEC-2001; 2001US-0337275P.
PR XX      (ABGE-) ABGENIX INC.
PA XX      Gudas J, Foltz I, Handa M, Gallo M;
PI DR      WPI; 2003-523295/49.
XX XX      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT PT      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX XX      intraepithelial squamous and glandular neoplasia or esophageal tumors.
PS PS      Example 2; SEQ ID NO 144; 89pp; English.
XX XX      The invention relates to a novel isolated monoclonal antibody (mAb)
CC CC      comprising a heavy chain polypeptide and light chain polypeptide having a
CC CC      sequence chosen from one of 53 fully defined amino acid sequences given
CC CC      in the specification, where the antibody specifically binds carbonic
CC CC      anhydrase IX (CA IX), tumour antigen. The antibody of the invention
CC CC      demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC CC      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC CC      cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC CC      tumour or breast cancer, possibly via gene therapy. The current sequence
CC CC      is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC CC      (heavy chain variable domain) protein of the invention. The protein was
CC CC      generated via the introduction of the human CA IX protein into a
CC CC      transgenic mouse strain.
SQ SQ      Sequence 120 AA:
Query Match          84.9%; Score 521; DB 7; Length 120;
Best Local Similarity 87.1%; Pred. No. 6.6e-37; Indels 4; Gaps 2;
Matches 101; Conservative 5; Mismatches 6;
QY 2 ESGPGLVKPKSQTSLNCTVSGGSIRSGGYWMWIROPKGKLEWIGIYHSGNTYNPSTL 61
DB 6 ESGGGLVKPKQSOTLSLTCTVGGGSISSGGYWMWSWRHGKGLMEIGIYYSGSYNPSTL 65
QY 62 KSRVTISVDTSKNHFLRSLSSVTAADTAVYYCARSDGT--LDNMWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKTLSSVTAADTAVYYCAR-DGNYNWYFDLMRGRLTVTVSS 120
RESULT 9
ADP03873
ID ADP03873 standard; protein; 120 AA.
AC ACP03873;
XX XX
XX XX      ADP03873;
DT DT      29-JUN-2004 (first entry)
DE DE      Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
KW KW      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW KW      cytoskeletal; colorectal neoplasm; renal cell carcinoma;
KW KW      cervical intraepithelial squamous neoplasia;
KW KW      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX XX      gene therapy; murine; mouse; human; heavy chain variable domain.
OS OS      Unidentified.
PN PN      WO2003048328-A2.
PD PD      12-JUN-2003.
PP PP      02-DEC-2002; 2002WKO-USO38550.
PF PF      03-DEC-2001; 2001US-0337275P.
PR PR      03-DEC-2001; 2001US-0337275P.
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XX (ABGE-) ABGENIX INC.
XX
XX Gudäs J, Foltz I, Handa M, Gallo M;
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 13; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumor antigen. The antibody of the invention
XX demonstrates cytosolic-activity and may be useful for treating a tumor,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumor or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 120 AA:
SQ
XX
XX Query Match 84.9%; Score 521; DB 7; Length 120;
XX Best Local Similarity 87.1%; Pred. No. 6.6e-37;
XX Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
XX
XX QY 2 ESGGGLVKSQTLSTCTVSGGSIKSGGYWMIKQPGKLEWIGYIHSGNTYNPSTL 61
XX DB 6 ESGGGLVKSQTLSTCTVSGGSIKSGGYWMIKQPGKLEWIGYIHSGNTYNPSTL 65
XX
XX QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR---SDGYTLDMNGGTLVTYSS 114
XX DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYVYCAR-DEINWYFDMRGTLVTYSS 120
XX
XX RESULT 10
XX ADP03977 ID ADP03977 standard; protein; 122 AA.
XX
XX AC ADP03977;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
XX
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumor antigen;
XX cytosolic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX OS Unidentified.
XX
XX PN MO2003048328-A2.
XX
XX PD 12-JUN-2003.
XX
XX PP 02-DEC-2002; 2002WO-US038550.
XX
XX PR 03-DEC-2001; 2001US-0337275P.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Gudäs J, Foltz I, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX

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```

XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 147; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumor antigen. The antibody of the invention
XX demonstrates cytosolic activity and may be useful for treating a tumor,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumor or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
XX Sequence 122 AA:
SQ
XX
XX Query Match 84.9%; Score 521; DB 7; Length 122;
XX Best Local Similarity 85.5%; Pred. No. 6.7e-37;
XX Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
XX
XX QY 2 ESGGGLVKSQTLSTCTVSGGSIKSGGYWMIKQPGKLEWIGYIHSGNTYNPSTL 61
XX DB 6 ESGGGLVKSQTLSTCTVSGGSIKSGGYWMIKQPGKLEWIGYIHSGNTYNPSTL 65
XX
XX QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR---SDGYTLDMNGGTLVTYSS 114
XX DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYVYCARVYDILTGCMVDWGQGTITVYSS 122
XX
XX RESULT 11
XX AAB36206 ID AAB36206 standard; protein; 473 AA.
XX
XX AC AAB36206;
XX
XX DT 15-FEB-2001 (first entry)
XX
XX DE Human immune system associated protein HISAP-4.
XX
XX KW Human; immune system associated protein; HISAP-4; immune disorder;
XX infection; autoimmune disease; cancer.
XX
XX OS Homo sapiens.
XX
XX PN US6135941-A.
XX
XX PD 24-OCT-2000.
XX
XX PP 27-MAR-1998; 98US-00049672.
XX
XX PR 27-MAR-1998; 98US-00049672.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Tang YT, Yue H, Lai P, Corley NC, Guejler KJ, Baughn MR;
XX Hillman JL, Au-Young J;
XX
XX WPI; 2001-030926/04.
XX
XX N-PSDB; AAC65522.
XX
XX New human immune system associated proteins (HISAP) and polynucleotides
XX encoding the HISAP, useful for diagnosing, treating or preventing immune
XX or cell proliferative disorders or infections.
XX
XX Claim 1; Col 53-56; 54pp; English.
XX

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QY      2  ESGPGLVPSQTLILCTCTVSGSIRSGGYWSWIRPGKGLWIGIYHSGNTYVNSL 61
DB      6  ESGPGLVPSQTLILCTCTVSGSIRSGGYWSWIRPGKGLWIGIYHSGNTYVNSL 65
QY      62 KSRVTMSVDTSKQNFSLRLSSVTAADTAIVYYCARSS--DGYTLDMWGCGTLVTVSS 114
DB      66 KSRVTISVDTSKQNFSLRLSSVTAADTAIVYYCARVLLMFGYMDVMWGCGTTVTVSS 121

RESULT 14
ADP03871
ID      ADP03871 standard; protein; 125 AA.
XX
XX      ADP03871;
XX
XX      29-JUL-2004 (first entry)
XX
XX      Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
XX
XX      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX      cytosol; colorectal neoplasm; renal cell carcinoma;
XX      cervical intraepithelial squamous neoplasia; oesophageal; breast cancer;
XX      cervical intraepithelial glandular neoplasia; heavy chain variable domain.
XX      gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX      Unidentified.
XX      OS
XX      PN      WO2003048328-A2.
XX
XX      PD      12-JUN-2003.
XX
XX      PF      02-DEC-2002; 2002WO-US038550.
XX
XX      PR      03-DEC-2001; 2001US-0337275P.
XX
XX      (ABGE-) ABGENIX INC.
XX
XX      PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
XX      WPI; 2003-523295/49.
XX
XX      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX      Claim 1; SEQ ID NO 11; 89pp; English.
XX
XX      The invention relates to a novel isolated monoclonal antibody (mab)
XX      comprising a heavy chain polypeptide and light chain polypeptide having a
XX      sequence chosen from one of 53 fully defined amino acid sequences given
XX      in the specification, where the antibody specifically binds carbonic
XX      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX      demonstrates cytosolic activity and may be useful for treating a tumour,
XX      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX      cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX      tumour or breast cancer, possibly via gene therapy. The current sequence
XX      is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX      (heavy chain variable domain) protein of the invention. The protein was
XX      generated via the introduction of the human CA IX protein into a
XX      transgenic mouse strain.
XX
XX      Sequence 125 AA;
XX
XX      Query Match      84.6%; Score 519.5; DB 7; Length 125;
XX      Best Local Similarity 83.3%; Pred. No. 9.2e-37;
XX      Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
```

```
DB      66 KSRVTISVDTSKQNFSLRLSSVTAADTAIVYYCARVYDFLTGYPAFDIMWGCGTMTVSS 125

RESULT 15
ADP03970
ID      ADP03970 standard; protein; 119 AA.
XX
XX      ADP03970;
XX
XX      29-JUL-2004 (first entry)
XX
XX      Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.
XX
XX      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX      cytosol; colorectal neoplasm; renal cell carcinoma;
XX      cervical intraepithelial squamous neoplasia;
XX      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX      gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX      Unidentified.
XX      OS
XX      PN      WO2003048328-A2.
XX
XX      PD      12-JUN-2003.
XX
XX      PF      02-DEC-2002; 2002WO-US038550.
XX
XX      PR      03-DEC-2001; 2001US-0337275P.
XX
XX      (ABGE-) ABGENIX INC.
XX
XX      PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
XX      WPI; 2003-523295/49.
XX
XX      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX      Example 2; SEQ ID NO 140; 89pp; English.
XX
XX      The invention relates to a novel isolated monoclonal antibody (mab)
XX      comprising a heavy chain polypeptide and light chain polypeptide having a
XX      sequence chosen from one of 53 fully defined amino acid sequences given
XX      in the specification, where the antibody specifically binds carbonic
XX      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX      demonstrates cytosolic activity and may be useful for treating a tumour,
XX      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX      cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX      tumour or breast cancer, possibly via gene therapy. The current sequence
XX      is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX      (heavy chain variable domain) protein of the invention. The protein was
XX      generated via the introduction of the human CA IX protein into a
XX      transgenic mouse strain.
XX
XX      Sequence 119 AA;
XX
XX      Query Match      84.3%; Score 517.5; DB 7; Length 119;
XX      Best Local Similarity 86.8%; Pred. No. 1.3e-36;
XX      Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
```

2 ESGPGLVPSQTLILCTCTVSGSIRSGGYWSWIRPGKGLWIGIYHSGNTYVNSL 61
6 ESGPGLVPSQTLILCTCTVSGSIRSGGYWSWIRPGKGLWIGIYHSGNTYVNSL 65
62 KSRVTMSVDTSKQNFSLRLSSVTAADTAIVYYCARSD-GYTLDMWGCGTTLVTVSS 114
66 KSRVTISVDTSKQNFSLRLSSVTAADTAIVYYCARGNYYGMDVMWGCGTTVTVSS 119

Search completed: August 30, 2006, 00:41:48
Job time : 104.427 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 / Search time 10.7091 Seconds

(without alignments)
1024.243 Million cell updates/sec

Title: US-10-027-725a-9

Perfect score: 614

Sequence: 1 LBSGPGLVKPSQTLSTLCTV.....RSDGYTLDMWGGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_80:*

2: PIR1:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501.5	81.7	135	2 S78051	Ig heavy chain pre
2	497.5	81.0	147	2 S13559	Ig heavy chain V r
3	492.5	80.2	140	2 I37782	Ig variable region
4	490	79.8	130	2 S30534	Ig heavy chain V r
5	488.5	79.6	116	2 S37456	Ig mu chain - huma
6	487.5	79.4	130	2 S31690	Ig heavy chain V r
7	480.5	78.3	121	2 S44113	Ig heavy chain V r
8	479.5	78.1	155	2 S31511	Ig heavy chain - h
9	477.5	77.8	146	2 S09710	Ig heavy chain V r
10	477.5	77.8	155	2 S31512	Ig heavy chain - h
11	473.5	77.1	146	2 S09711	Ig heavy chain V r
12	472.5	77.0	127	2 S19668	Ig heavy chain V r
13	472.5	77.0	128	2 S31514	Ig heavy chain - h
14	472	76.9	137	2 S31676	Ig heavy chain V r
15	469	76.4	99	2 S26803	Ig heavy chain V r
16	467.5	76.1	123	2 S30530	Ig heavy chain V r
17	467	76.1	99	2 S26801	Ig heavy chain V r
18	467	76.1	122	2 S69912	Ig V-D-J region (N
19	465	75.7	139	2 S31586	Ig heavy chain V r
20	464	75.6	99	2 S26802	Ig heavy chain V r
21	461	75.1	145	2 S78055	Ig heavy chain pre
22	460.5	75.0	109	2 PH1673	Ig heavy chain V r
23	459	74.8	110	2 S44110	Ig heavy chain V-D
24	458	74.6	139	2 A41210	Ig heavy chain pre
25	457	74.4	118	2 A26340	Ig heavy chain V-I
26	454	73.9	99	2 S26839	Ig heavy chain V r
27	454	73.9	99	2 S26839	Ig heavy chain V r
28	452	73.6	135	2 S31604	Ig heavy chain V r
29	451	73.5	118	2 S20780	Ig heavy chain V r

30	451	73.5	129	2 S44114	Ig heavy chain V r
31	448	73.0	99	2 S12418	Ig heavy chain V r
32	447.5	72.9	139	2 S31696	Ig heavy chain V r
33	445.5	72.6	137	2 S31585	Ig heavy chain V r
34	445.5	72.6	140	2 A49045	Ig heavy chain V r
35	445	72.5	120	2 PT0370	Ig mu chain precu
36	444	72.3	126	2 S47010	Ig heavy chain V4.
37	443	72.1	99	2 S26800	Ig heavy chain V r
38	442	72.0	105	2 S44125	Ig heavy chain V r
39	442	72.0	105	2 S44125	Ig lambda chain V
40	442	72.0	118	2 S24443	Ig heavy chain V r
41	442	72.0	140	2 S78052	Ig heavy chain pre
42	441.5	71.9	98	2 S12421	Ig heavy chain V r
43	441.5	71.9	132	2 A38911	Ig heavy chain V r
44	441.5	71.9	140	2 A24770	hypothetical hybr
45	441	71.8	97	2 S26906	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S78051 Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_rev15ion 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051, S23716

R/Hairdinatnath, N.
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 <HAR>

A/Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:g37814; PIDN:CA38306.1; PID R/Hairdinatnath, N.; Goldfarb, I.S.; Ikematsu, H.; Butastero, S.E.; Wilder, R.L.; Nockins, Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A/Molecule type: mRNA

A/Residues: 13-111 <HAW>

A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_rev15ion 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051, S23716

R/Hairdinatnath, N.
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 <HAR>

A/Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:g37814; PIDN:CA38306.1; PID R/Hairdinatnath, N.; Goldfarb, I.S.; Ikematsu, H.; Butastero, S.E.; Wilder, R.L.; Nockins, Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A/Molecule type: mRNA

A/Residues: 13-111 <HAW>

A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437

C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_rev15ion 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051, S23716

R/Hairdinatnath, N.
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 <HAR>

A/Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:g37814; PIDN:CA38306.1; PID R/Hairdinatnath, N.; Goldfarb, I.S.; Ikematsu, H.; Butastero, S.E.; Wilder, R.L.; Nockins, Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <MOR>
A:Cross-references: UNIPARC:UP10000115EB5; EMBL:X56158; NID:937724; PIDN:CAA39626.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;
Best Local Similarity 82.8%; Pred. No. 7e-38;
Matches 96; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

Oy 2 ESGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 61
Db 32 ESGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 91

Oy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG-----GYTLDMWGQGLTVTVSS 114
Db 92 KSRVTISVDTSKNHFSLRLSSVTADTAIVYVCARPLMFGELFDYWGQGLTVTVSS 147

RESULT 3

I37782
Ig variable region (VDJ) (clone T23-9) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: J37782; S25476
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A36876; MUID:9411917; PMID:8290556
A:Accession: J37782

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: UNIPARC:UP10000176E83; EMBL:X67906; NID:933562; PIDN:CAA48104.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 492.5; DB 2; Length 140;
Best Local Similarity 82.2%; Pred. No. 1.9e-37;
Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

Oy 2 ESGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 61
Db 25 ESGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 82

Oy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG-----GYTLDMWGQGLTVTVSS 114
Db 83 KSRVTISVDTSKNHFSLRLSSVTADTAIVYVCARHSSSWYGRYPDYWGQGLTVTVSS 140

RESULT 4

S30534
Ig heavy chain V region - human

C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C:Accession: S30534
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <MAR>
A:Cross-references: UNIPARC:UP10000113F45; EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 490; DB 2; Length 130;
Best Local Similarity 78.4%; Pred. No. 2.9e-37;
Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

Oy 2 ESGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 61
Db 6 ESGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 65

Oy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG-----GYTLDMWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAIVYVCARPLMFGELFDYWGQGLTVTVSS 147

Oy 110 VTVSS 114
Db 126 VTVSS 130

RESULT 5

S37456
Ig mu chain - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37456
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A:Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from f
A:Reference number: S37453
A:Accession: S37456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <MCI>
A:Cross-references: UNIPARC:UP100001161C0; EMBL:X75024; NID:9404313; PIDN:CAA52932.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 488.5; DB 2; Length 116;
Best Local Similarity 81.2%; Pred. No. 3.5e-37;
Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

Oy 6 GLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 65
Db 1 GLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 60

Oy 66 TMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG-----LDNWGQGLTVTVSS 114
Db 61 TISVDTSKNHFSLRLSSVTADTAIVYVCARG-GYSYGYYYVYDYGKGTIVTVSS 116

RESULT 6

S31690
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31690
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the f
A:Reference number: S31585
A:Accession: S31690
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <CUI>
A:Cross-references: UNIPARC:UP10000116471; EMBL:Z14199; NID:930984; PIDN:CAA78566.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 130;
Best Local Similarity 78.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

Oy 2 ESGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 61
Db 11 ESGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLIEWIGYIYHSGNTYNNPSL 68

C/Accession: S09711
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A/Reference number: S09710; MUID:90262535; PMID:2111699
A/Accession: S09711
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-146 <HUG>
A/Cross-references: UNIPARC:UPI0000176CD3
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;
Best Local Similarity 73.8%; Pred. No. 1e-35;
Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 61
D 25 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 84
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCAR-----SDGYTLDNWGQGLTVTV 112
D 85 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARVLVSRYSISQYSYMDVWGKTTVTV 144
QY 113 SS 114
D 145 SS 146

RESULT 12

S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C/Accession: S19668; S24445
R/Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19668
A/Molecule type: mRNA
A/Residues: 1-127 <MAR>
A/Cross-references: UNIPARC:UPI0000176C7F; EMBL:X61648
R/Jones, P.T.
submitted to the EMBL Data Library, October 1991
A/Reference number: S24442
A/Accession: S24445
A/Molecule type: mRNA
A/Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F', <JON>
A/Cross-references: UNIPARC:UPI0000115FE7; EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;
Best Local Similarity 74.6%; Pred. No. 1e-35;
Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 61
D 6 QSGGGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDG-----YTLDNWGQGLTVTV 112
D 66 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDG-----YTLDNWGQGLTVTV 125
QY 113 SS 114
D 126 SS 127

RESULT 13

S31514
Ig heavy chain - human

C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31514
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-
A/Reference number: S31509
A/Accession: S31514
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <CHA>
A/Cross-references: UNIPARC:UPI00001160FB; EMBL:X69862; NID:933086; PIDN:CAA49496.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;
Best Local Similarity 78.4%; Pred. No. 1e-35;
Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 61
D 13 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 72
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCAR-----SDGYTLDNWGQGLTVTVSS 114
D 73 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARIGVNGYGRDPWGQGLTVTVSS 128

RESULT 14

S31676
Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31676
R/Cisniew, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31676
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-137 <CUI>
A/Cross-references: UNIPARC:UPI0000116461; EMBL:Z14182; NID:931031; PIDN:CAA78551.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;
Best Local Similarity 82.6%; Pred. No. 1.3e-35;
Matches 99; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 61
D 25 ESGPGLVPSQTLSTCTVSGGSIRSGGYWMIROPPGKGLWIGYIYHSGNTYNNPSL 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDG-----YTLDNWGQGLTVTVSS 114
D 83 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDG-----YTLDNWGQGLTVTVSS 137

RESULT 15

S26803
Ig heavy chain V region - human

C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26803
R/Meng, N.; Snyder, J.G.; Yu-Lee, L.; Marcuse, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.

A:Reference number: S26800; MUID:92201299; PMID:1348029
 A:Accession: S26803
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-99 <MEN>
 A:Cross-references: UNIPARC:UPI0000116485; EMBL:Z14238; NID:937710; PIDN:CAA78607.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 99;
 Best Local Similarity 92.6%; Pred. No. 1.7e-35;
 Matches 87; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY	2	ESGPGLVKPSQTLSTCTVSGSGSIRSGGYTWSMIRDPGKGLWIGYTHSGNTYYNPSL	61
Db	6	ESGPGLVKPSQTLSTCTVSGSGSIRSGDYTWSMIRDPGKGLWIGYTHSGNTYYNPSL	65
QY	62	KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYYCAR	95
Db	66	KSRVTISVDTSKNQFSLKLSSVTADTAADTAAYYCAR	99

Search completed: August 30, 2006, 00:42:54
 Job time : 11.7091 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 62.1818 Seconds
(without alignments)
1695.862 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LBSGPGLVKPSQTLSTLCTV.....RSDGYTLDMWGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 2849598 segs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504.5	82.2	476	2	06GMX1_HUMAN
2	480	78.2	465	2	06GMX6_HUMAN
3	480	78.2	478	2	Q7Z379_HUMAN
4	470.5	76.6	119	2	Q9UL73_HUMAN
5	469.5	76.5	492	2	Q7Z374_HUMAN
6	469	76.4	477	2	06GMX7_HUMAN
7	468	76.2	150	2	Q95973_HUMAN
8	460	74.9	496	2	096KX8_HUMAN
9	460	74.9	620	2	096KX8_HUMAN
10	452	73.6	576	2	Q6P418_HUMAN
11	441	71.8	139	2	086SX2_HUMAN
12	439.5	71.6	129	1	HV2F_HUMAN
13	431	70.2	130	2	081ZD7_HUMAN
14	429.5	70.0	595	2	08MTX4_HUMAN
15	429.5	70.0	597	2	06GMX5_HUMAN
16	429.5	70.0	597	2	Q9BU10_HUMAN
17	429.5	70.0	625	2	Q96AA6_HUMAN
18	425.5	69.3	597	2	Q9BOB8_HUMAN
19	424.5	69.1	478	2	Q6NYH3_HUMAN
20	420	68.4	146	1	HV21_HUMAN
21	412	67.1	473	1	Q8TC63_HUMAN
22	393.5	64.1	117	1	HV2G_HUMAN
23	393	64.0	483	2	Q5U413_MOUSE
24	392.5	63.9	479	2	Q99M22_MOUSE
25	389	63.4	116	2	Q7Z376_HUMAN
26	387	63.0	136	2	Q6LBD5_MOUSE
27	377.5	61.5	476	2	Q6MZ97_HUMAN
28	377.5	61.5	615	2	Q659B6_RAT
29	375.5	61.2	119	2	Q53VR3_MOUSE
30	372.5	60.7	137	1	HV46_MOUSE
31	370.5	60.3	262	2	Q65Z11_MOUSE

32	369.5	60.2	590	2	Q569B8_RAT	Q569B8_rattus norv
33	368.5	60.0	477	2	Q510J1_RAT	Q510J1_rattus norv
34	367.5	59.9	115	2	Q53VQ1_MOUSE	Q53VQ1_mus musculu
35	365.5	59.5	119	2	Q53VQ5_MOUSE	Q53VQ5_mus musculu
36	364	59.3	122	2	Q9UL75_HUMAN	Q9UL75_homo sapien
37	361	58.8	120	2	Q53VR7_MOUSE	Q53VR7_homo sapien
38	357.5	58.2	113	1	HV47_MOUSE	P01823_mus musculu
39	353.5	57.6	98	2	Q53VR2_MOUSE	Q53VR2_mus musculu
40	353.5	57.6	119	2	Q53VQ9_MOUSE	Q53VQ9_mus musculu
41	352	57.3	485	2	Q561M5_MOUSE	Q561M5_mus musculu
42	349.5	56.9	144	1	HV43_MOUSE	P01819_mus musculu
43	348.5	56.8	116	1	HV61_MOUSE	P18532_mus musculu
44	348	56.7	591	2	Q510L9_RAT	Q510L9_rattus norv
45	347	56.5	117	1	HV62_MOUSE	P18533_mus musculu

ALIGNMENTS

RESULT 1
06GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
ID 06GMX1_HUMAN
AC 06GMX1;
DT 19-JUL-2004, integrated into UniProtKB/TREMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smilins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC
EMBL: BC073773; AAT73773.1; -; mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 3.

DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGL; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KW SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 82.2%; Score 504.5; DB 2; Length 476;
 Best Local Similarity 76.6%; Pred. No. 1.3e-43;
 Matches 95; Conservative 12; Mismatches 4; Indels 13; Gaps 2;

QY 2 ESGGGLVPSQTLSTLTCTVSGSGSIRSGGYWSWIRPPGKGLWIGYIYHSGNTYVPSL 61
 DB 25 ESGGGLVPSQTLSTLTCTVSGSGSIRSGGYWSWIRPPGKGLWIGYIYHSGNTYVPSL 84
 QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGQGLTVVSS 110
 DB 85 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGQGLTVVSS 142
 QY 111 TVSS 114
 DB 143 TVSS 146

RESULT 2

06GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
 AC 06GMX6;
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins L.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscii T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield A.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RL Strausberg R.;
 CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC EMBL; BC073766; AAH73766.1; -, mRNA.
 DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGL; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KW SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 78.2%; Score 480; DB 2; Length 465;
 Best Local Similarity 84.1%; Pred. No. 4.4e-41;
 Matches 95; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

QY 2 ESGGGLVPSQTLSTLTCTVSGSGSIRSGGYWSWIRPPGKGLWIGYIYHSGNTYVPSL 61
 DB 25 ESGGGLVPSQTLSTLTCTVSGSGSIRSGGYWSWIRPPGKGLWIGYIYHSGNTYVPSL 82
 QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGQGLTVVSS 114
 DB 83 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGQGLTVVSS 135

RESULT 3

072379_HUMAN PRELIMINARY; PRT; 478 AA.
 AC 072379;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Hypothetical protein DKFP666K04218 (Fragment).
 GN Name=DKFP666K04218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC EMBL; BX538066; CAD97996.1; -, mRNA.
 DR HSP; P01820; 167J.
 DR SMK; Q72379; 248-456.
 DR Ensemble; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGL; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein; Immunoglobulin domain; Repeat.
 FT NON TRP 1
 SQ SEQUENCE 478 AA; 51620 MW; 4AFB541F3217CA1 CRC64;

Query Match 78.2%; Score 480; DB 2; Length 478;
 Best Local Similarity 77.4%; Pred. No. 4.6e-41;

Matches 89; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
DB 24 ESGPGLVKPSQTLSTLCTVSGSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYNPSTL 83

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGY--TLDNMGQGLTVTVSS 114
DB 84 ESRLLSISIDTSKNQFSLRLNLSLTAAADTAVYFCARGVGLGTAFIMWGQGLTVTVSS 138

RESULT 4
Q9UL73 HUMAN PRELIMINARY; PRT; 119 AA.

AC Q9UL73
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9207875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,
RA Diamond B.,
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiootype."
RT J. Exp. Med. 174:1639-1652(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90059975; PubMed=2511001;
RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.,
RT "The smaller human VH gene families display remarkably little
RT polymorphism."
RT EMBO J. 8:3741-3748(1989).
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CC EMBL: AF035041; AAD56277.1; -; mRNA.
DR PIR: P08076; P08076.
DR PIR: S12416; S12416.
DR HSSP: P01820; IGTJ.
DR SMR: Q9UL73; 2-119.
DR Linkhub; Q9UL73;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD88686420EAOBE CRC64;

Query Match 76.6%; Score 470.5; DB 2; Length 119;
Best Local Similarity 79.3%; Pred. No. 9,4e-41;
Matches 92; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYNPSTL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG--YTLDMNGQGLTVTVSS 114
DB 64 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYFCARGVGLGTAFIMWGQGLTVTVSS 119

RESULT 5
Q7Z374 HUMAN PRELIMINARY; PRT; 492 AA.

AC Q7Z374
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amdt C., Osanger A.,
RA Fobo G., Han M., Wiemann S.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC EMBL: BX538077; CAD98001.1; -; mRNA.
DR HSSP: P01820; IGTJ.
DR SMR: Q7Z374; 262-470.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT NON_TER 492
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 76.5%; Score 469.5; DB 2; Length 492;
Best Local Similarity 76.9%; Pred. No. 5,8e-40;
Matches 90; Conservative 10; Mismatches 12; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
DB 37 ESGPGLVKPSQTLSTLCTVSGSGSVSNRNRYWGIROPPGKGLWIGIYHSGNTYNPSTL 96

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAR---SDGYTLDMNGQGLTVTVSS 114
DB 97 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYCYRHHEGPGYW-FDPMGQGLTVTVSS 152

RESULT 6
Q6GKX7 HUMAN PRELIMINARY; PRT; 477 AA.

AC Q6GKX7
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.

OS Homo sapiens (Human).
 OC Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Primary B-Cells;
 RC MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Primary B-Cells;
 RC Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC073765; AAHT3765.1; -, mRNA.
 DR SMR: O6GMX7; 247-455.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG1; 1.
 DR SMART; SM00407; IG1; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;
 Query Match 76.4%; Score 469; DB 2; Length 477;
 Best Local Similarity 80.0%; Pred. No. 6.3e-40;
 Matches 92; Conservative 6; Mismatches 13; Indels 4; Gaps 2;
 QY 2 ESGPGLVKSQTLSTCTVSGSIRSGGYWSWIRQPGKGLMIGYVHSGNTYVNSL 61
 DB 25 ESGGLVKSPTSLTCTVSGSIS--YWSWIRQTKGLMIGYVSHSGSTYVNSL 82
 QY 62 KSRVTVSDTSKNHPSRLSSVTAAADTAAYVYCARSDG--YTLDMWGQGTLYTVSS 114
 DB 83 KSRVTVSDTSKNHPSRLSSVTAAADTAAYVYCARSDG--YTLDMWGQGTLYTVSS 137
 RESULT 7
 ID 095973 HUMAN PRELIMINARY; PRT; 150 AA.
 AC 095973;
 NCBI_TaxID=9606;

DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1999, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE V4 heavy chain variable region precursor (Fragment).
 DE
 GN Name=IGM;
 OS Homo sapiens (Human).
 OC Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
 RT "Clonal proliferation of IGM secreting B cell in the synovium of
 RT Babeset's patient with arthritis."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=9201262; PubMed=1718404;
 RA Haridranath N., Goldfarb I.S., Ikematsu H., Burastero S.E.,
 RA Wilder R.L., Norkins A.L., Casali P.;
 RT "Complete sequence of the genes encoding the VH and VL regions of low-
 RT and high-affinity monoclonal IGM and IGA1 rheumatoid factors produced
 RT by CD5+ B cells from a rheumatoid arthritis patient."
 RL Int. Immunol. 3:865-875(1991).
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 CC -----
 CC EMBL: AF103795; AAC79084.1; -, mRNA.
 DR PIR; S31673; S31673.
 DR PIR; S78056; S78056.
 DR HSSP; P01820; 1G7J.
 DR SMR; O95973; 20-147.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR013106; V-set.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin domain; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 >150 V4 heavy chain variable region.
 FT NON TER 150 150
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
 Query Match 76.2%; Score 468; DB 2; Length 150;
 Best Local Similarity 78.8%; Pred. No. 2.2e-40;
 Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
 QY 2 ESGPGLVKSQTLSTCTVSGSIRSGGYWSWIRQPGKGLMIGYVHSGNTYVNSL 61
 DB 25 ESGGLVKSPTSLTCTVSGSISSTNYWGIRQPPKGLMIGYVSHSGSDYVNSL 84
 QY 62 KSRVTVSDTSKNHPSRLSSVTAAADTAAYVYCARSDG--YTLDMWGQGTLYTVSS 114
 DB 85 KSRVTVSDTSKNHPSRLSSVTAAADTAAYVYCARSDG--YTLDMWGQGTLYTVSS 137
 RESULT 8
 ID 096KX8 HUMAN PRELIMINARY; PRT; 496 AA.
 AC 096KX8;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE MGC27165 protein.
 DE
 OS Homo sapiens (Human).
 OC Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 EMBL: BC016369; AA016369.1; -; mRNA.
 HSSP: P01876; 10W0.
 DR SMR; Q96KX8; 266-474.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_MHC; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 496 AA; 53392 MW; D346929849040D69 CRC64;
 Query Match 74.9%; Score 460; DB 2; Length 496;
 Best Local Similarity 75.0%; Pred. No. 5.7e-39;
 Matches 90; Conservative 8; Mismatches 14; Indels 8; Gaps 2;
 QY 2 EGGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPPGKGLWIGVYHSGNTYVPSL 61
 DB 25 EGGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPPGKGLWIGVYHSGNTYVPSL 84
 QY 62 KSRVTVSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGYT-----LDNWGGGLTVTVSS 114
 DB 85 KSRVTVSVDTSKNHFSLRLSSVTAAADTAAYVYCAR-HGYSSRGRTGALDYWGQGLTVTVSS 143
 RESULT 9
 Q96EYO HUMAN PRELIMINARY; PRT; 620 AA.
 AC Q96EYO;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 05-JUN-2004, sequence version 2.
 DT 07-FEB-2006, entry version 26.
 DE IGHW protein.
 GN Name=IGHW;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo
 NC NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Primary B-Cells;
 RC NIH MGC Project;
 RG Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RA [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91252286; PubMed=1904154;
 RA Neale G.A., Kitchingman G.R.;
 RT "RNA transcripts initiating within the human immunoglobulin mu heavy
 chain enhancer region contain a non-translatable exon and are
 RT extremely heterogeneous at the 5' end.";
 RL Nucleic Acids Res. 19:2427-2433(1991).
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 CC
 EMBL: BC011857; AA011857.2; -; mRNA.
 DR PIR; S15590; S15590.
 DR HSSP; P01820; 1G7J.
 DR SMR; Q96EYO; 27-251.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_MHC; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 620 AA; 66125 MW; 990A1AA468BF27B CRC64;
 Query Match 74.9%; Score 460; DB 2; Length 620;
 Best Local Similarity 80.5%; Pred. No. 7.3e-39;
 Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps 3;
 QY 2 EGGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPPGKGLWIGVYHSGNTYVPSL 61
 DB 32 EGGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPPGKGLWIGVYHSGNTYVPSL 89

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGTLDN-----WGQGLTVTVSS 114
Db 90 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCA-SQWELPTVGLFTWGGTLTVTVSS 146

RESULT 10
Q6P418_HUMAN PRELIMINARY; PRT; 576 AA.
ID Q6P418_HUMAN
AC Q6P418
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 21-FEB-2006, entry version 20.
DE IGHG protein.
GN Name-IGHG;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.V., Scheetz T.E.,
RA Brownstein M.J., Umed T.B., Toshitsugu S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-cells;
RA Strausberg R.L.
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BC063384; AAH63384.1; -; mRNA.
DR HSSP: P01820; 1A7N.
DR Ensembl: ENSG00000196122; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG-CL.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR InterPro: IPR013151; Immunoglobulin.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; CI-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGH1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63364 MW; FBB97C949D720F1E CRC64;

Query Match 73.6%; Score 452; DB 2; Length 576;
Best Local Similarity 77.6%; Pred. No. 4.6e-38;
Matches 90; Conservative 6; Mismatches 16; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWMIKPPKGLGEMIGIYHSGNTYVPSL 61
Db 32 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWMIKPPKGLGEMIGIYHSGNTYVPSL 90

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDG---YTLDNWGQGLTVTVSS 114
Db 91 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSLGDIYYGMDVWGQGLTVTVSS 146

RESULT 11
Q66SX2_HUMAN PRELIMINARY; PRT; 139 AA.
ID Q66SX2_HUMAN
AC Q66SX2
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DE 07-FEB-2006, entry version 14.
DE Full-length cDNA clone CS0DL004YMI9 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.,
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B cells;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BX248300; CAD62627.1; -; mRNA.
DR HSSP: P01820; 1G7J.
DR SMR: Q66SX2; 34-132.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003596; IG_V.
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 71.8%; Score 441; DB 2; Length 139;
Best Local Similarity 89.4%; Pred. No. 1.3e-37;
Matches 84; Conservative 5; Mismatches 3; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWMIKPPKGLGEMIGIYHSGNTYVPSL 61
Db 38 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWMIKPPKGLGEMIGIYHSGNTYVPSL 95

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCAR 95
Db 96 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCAR 129

RESULT 12
H2V2F_HUMAN STANDARD; PRT; 129 AA.
ID H2V2F_HUMAN
AC P01824
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 36.
DE Ig heavy chain V-II region WH4.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN
RP PROTEIN SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debutre B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma
protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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CC
CC PIR: A02099; D2HUMA.
DR PDB: 1ZVO; X-ray; C/D=--.
DR SMR: P01824; 2-129.
DR GlycositeDB: P01824; --.
DR GO: GO:0005576; Cellular region; NAs.
DR GO: GO:0003823; Antigen binding; NAs.
DR GO: GO:0006955; Immune response; NAs.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF00409; V-set; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; Ig_Like; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >129
FT Ig heavy chain V-II region WAA.
FT /FTID=PRO_0000059912.
FT DOMAIN 1 113
FT NON_TER 129 129 Ig-like.
FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
SQ
Query Match 71.6%; Score 439.5; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 1,7e-37;
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVWSIRQPPGKGLFWIGYIHSGNTYNSPL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVWSIRQPPGKGLFWIGYIHSGNTYNSPL 65
QY 62 KSRVYMSVPTSKNHFSLRLSSVTAADTAAYVYCAR-----SDGYTLDMNGQGT 108
DB 66 KSRVYMSVPTSKNHFSLRLSSVTAADTAAYVYCAR-----SDGYTLDMNGQGT 123
QY 109 LVTVSS 114
DB 124 TVTVSS 129
RESULT 13
Q81ZD7 HUMAN PRELIMINARY; PRT; 130 AA.
AC Q81ZD7
ID Q81ZD7 HUMAN
DT 01-MAR-2003. Integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003. sequence version 1.
DT 07-FEB-2006. entry version 15.
DE Anti-chryoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Jiang Y.-J., Chung J., Park J.-Y.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL: AY145445; AAN64329.1; --; mRNA.
DR HSSP: P01820; 1G7J.
DR SMR: Q81ZD7; 1-130.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; Ig_Like; 1.
KW Immunoglobulin domain.
FT CHAIN 1 130
FT NON_TER 130 130
FT SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;
SQ
Query Match 70.2%; Score 431; DB 2; Length 130;
Best Local Similarity 71.2%; Pred. No. 1.3e-36;
Matches 89; Conservative 8; Mismatches 16; Indels 12; Gaps 4;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYVWSIRQPPGKGLFWIGYIHSGNT-----Y 56
DB 6 QSGPGLVKPSQTLSTCTVSGGSIIRSGYVWSIRQPPGKGLFWIGYIHSGNTYNSPL 65
QY 57 YNPSLRSRYTMSVDYTSKNHFSRLSSVTAADTAAYVYCAR-----SDG--YT-LDMNGQGT 109
DB 66 YNPSLRSRYTMSVDYTSKNHFSRLSSVTAADTAAYVYCAR-----SDG--YT-LDMNGQGT 125
QY 110 VTVSS 114
DB 126 VTVSS 130
RESULT 14
Q8WDX4 HUMAN PRELIMINARY; PRT; 595 AA.
ID Q8WDX4 HUMAN
AC Q8WDX4
DT 01-MAR-2002. Integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004. sequence version 2.
DT 07-FEB-2006. entry version 24.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marcusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;

```

RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Lymph;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99235232; PubMed=2497188;
RA Sanz I., Casali P., Thomas J.W., Nockins A.L., Capra J.D.;
RT "Nucleotide sequences of eight human natural autoantibody VH regions
RT reveals apparent restricted use of VH families.";
RL J. Immunol. 142:4054-4061(1989).
CC -----
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CC -----
DR EMBL: BC019235; AAH19235.2; -, mRNA.
DR PIR: G34964; G34964.
DR HSSP: P01861; 1ADQ.
DR SMR: Q8WDX4; 27-256.
DR Ensembl: ENSG00000130076; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 4.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
DR Hypothetical protein.
SQ SEQUENCE 595 AA; 65291 MW; 0D4B50776545714E CRC64;

Query Match 70.0%; Score 429.5; DB 2; Length 595;
Best Local Similarity 72.5%; Pred. No. 1e-35;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVKPSQTLSTCTVSGSIRSGYWSWIRQPGKGLGEMIGIYHSGNTYVNSLKS 63
DB 34 GAGILKPSERTSLTCGVYGSF--SGYWSWIRQPGKGLGEMIGIYHSGNTYVNSLKS 91
QY 64 RVTISVDTSKKHPSRLSSVTADTAIVYCAR-----SDG-YTLDMWGQGLTVVSS 114
DB 92 RVTISVDTSKKHPSRLSSVTADTAIVYCAR-----SDG-YTLDMWGQGLTVVSS 151

RESULT 15
Q6GMX5 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q6GMX5.
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
OX NCBI [1]
RN NUCLEOTIDE SEQUENCE.
RC Tissue=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Groue L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Strapleno M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Lymph;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC073767; AAH73767.1; -, mRNA.
DR SMR: Q6GMX5; 20-249.
DR Ensembl: ENSG00000130076; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 4.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65305 MW; 2A1E75FEAD85230 CRC64;

Query Match 70.0%; Score 429.5; DB 2; Length 597;
Best Local Similarity 72.5%; Pred. No. 1e-35;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVKPSQTLSTCTVSGSIRSGYWSWIRQPGKGLGEMIGIYHSGNTYVNSLKS 63
DB 27 GAGILKPSERTSLTCGVYGSF--SGYWSWIRQPGKGLGEMIGIYHSGNTYVNSLKS 84
QY 64 RVTISVDTSKKHPSRLSSVTADTAIVYCAR-----SDG-YTLDMWGQGLTVVSS 114
DB 85 RVTISVDTSKKHPSRLSSVTADTAIVYCAR-----SDG-YTLDMWGQGLTVVSS 144

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Search completed: August 30, 2006, 00:35:15
 Job time : 63.1818 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 15.5455 Seconds
(without alignments)
641.891 Million cell updates/sec

Title: US-10-027-725a-9

Sequence: 1 LBSGPGIYKPSQTLSTCTV.....RSDGYTLDMWGQGLTVTSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents_AA:*
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2: /EMC_Celerra_SIDS3/prodata/2/1aa/6 COMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/1aa/7 COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/8 COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/1aa/9 COMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/1aa/10 COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/11 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	2	US-09-049-672A-4
2	515.5	84.0	117	2	US-10-330-613A-13
3	508	82.7	172	2	US-09-472-087-7
4	508	82.7	172	2	US-09-472-087-86
5	507.5	82.7	117	2	US-10-330-613A-5
6	502.5	81.8	119	2	US-09-025-769B-39
7	502.5	81.8	119	2	US-09-025-769B-65
8	502.5	81.8	119	2	US-09-490-070A-39
9	502.5	81.8	119	2	US-09-490-070A-65
10	502.5	81.8	119	2	US-09-490-153-39
11	502.5	81.8	119	2	US-09-490-153-65
12	502.5	81.8	119	2	US-09-490-324-39
13	502.5	81.8	119	2	US-09-490-324-65
14	497.5	81.0	119	2	US-10-330-613A-25
15	496	80.8	122	1	US-08-360-125-11
16	496	80.8	122	1	US-08-450-578-11
17	496	80.8	122	1	US-09-017-628-11
18	496	80.8	122	1	US-09-014-880-11
19	496	80.8	122	2	US-08-450-363-11
20	496	80.8	122	2	US-09-467-903-11
21	494.5	80.5	121	2	US-10-330-613A-37
22	492.5	80.2	117	2	US-09-720-493-2
23	492.5	80.2	117	2	US-10-330-613A-33
24	492	80.1	467	2	US-09-800-729-145
25	491	80.0	118	2	US-09-025-769B-25
26	491	80.0	118	2	US-09-490-070A-25

27	491	80.0	118	2	US-09-490-153-25	Sequence 25, Appl
28	491	80.0	118	2	US-09-490-324-25	Sequence 20, Appl
29	491	80.0	120	2	US-09-424-840B-20	Sequence 25, Appl
30	487.5	79.4	119	1	US-08-360-125-5	Sequence 5, Appl
31	487.5	79.4	119	1	US-08-450-578-5	Sequence 5, Appl
32	487.5	79.4	119	1	US-09-017-628-5	Sequence 5, Appl
33	487.5	79.4	119	1	US-09-014-880-5	Sequence 5, Appl
34	487.5	79.4	119	1	US-08-450-363-5	Sequence 5, Appl
35	487.5	79.4	119	2	US-09-467-903-5	Sequence 5, Appl
36	482.5	78.6	121	2	US-10-330-613A-9	Sequence 9, Appl
37	481.5	78.4	121	2	US-10-330-613A-17	Sequence 1, Appl
38	481.5	78.4	121	2	US-10-330-613A-17	Sequence 1, Appl
39	472	76.9	244	2	US-08-918-148-79	Sequence 79, Appl
40	472	76.9	244	2	US-09-138-091A-77	Sequence 77, Appl
41	469	76.4	99	2	US-10-194-975-38	Sequence 38, Appl
42	467	76.1	99	2	US-10-194-975-36	Sequence 36, Appl
43	467	76.1	99	2	US-10-194-975-39	Sequence 35, Appl
44	467	76.1	99	2	US-10-330-613A-45	Sequence 45, Appl
45	467	76.1	99	2	US-10-330-613A-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

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LIBRARY: PANCTUT01
CLONE: 1513264
US-09-049-672a-4

Query Match      84.9%; Score 521; DB 2; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.5e-44;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

Qy 2 ESGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 61
Db 25 ESGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 84

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSD-----GYTLDMWGCGTLVTYSS 114
Db 85 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGCGTLVTYSS 143

RESULT 2
US-10-330-613A-13
Sequence 13, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match      84.0%; Score 515.5; DB 2; Length 117;
Best Local Similarity 86.8%; Pred. No. 1.7e-44;
Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;

Qy 2 ESGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 61
Db 6 ESGGLVPSQTLSTLCTVSGGSIRSGGYWTWIRPPGKLEWIGYIYHSGNTYVNSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGCGTLVTYSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGCGTLVTYSS 117

RESULT 3
US-09-472-087-7
Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      82.7%; Score 508; DB 2; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 3 SGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 62
Db 1 SGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 60

Qy 63 SRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG--YTLDMWGCGTLVTYSS 114
Db 61 SRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGCGTLVTYSS 114

RESULT 4
US-09-472-087-86
Sequence 86, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      82.7%; Score 508; DB 2; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy 3 SGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 62
Db 1 SGGLVPSQTLSTLCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 60

Qy 63 SRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG--YTLDMWGCGTLVTYSS 114
Db 61 SRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYTLDMWGCGTLVTYSS 114

RESULT 5
US-10-330-613A-5
Sequence 5, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
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US-10-330-613A-5

82.7%; Score 507.5; DB 2; Length 117;

Query Match
Best Local Similarity 86.8%; Pred. No. 1.1e-43;
Matches 99; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLMWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLMWIGIYHSGNTYNNPSL 65
QY 62 KSRVTVSVDTSKNHFSLRLSSVTAADTAAYYCAR--SDGYTLDMWGCGTLTVTVSS 114
DB 66 KSRVTVSVDTSKNHFSLRLSSVTAADTAAYYCAR--SDGYTLTVSS 117

RESULT 6

US-09-025-769B-39
Sequence 39, Application US/09025769B

Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: US/09/025,769B
PRIORITY APPLICATION DATA:
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: EP 95 11 3021.0
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;
QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLMWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLMWIGIYHSGNTYNNPSL 63
QY 62 KSRVTVSVDTSKNHFSLRLSSVTAADTAAYYCAR--SDGYTLDMWGCGTLTVTVSS 114
DB 64 KSRVTVSVDTSKNHFSLRLSSVTAADTAAYYCAR--SDGYTLTVSS 119

RESULT 7

US-09-025-769B-65
Sequence 65, Application US/09025769B

Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: US/09/025,769B
PRIORITY APPLICATION DATA:
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: EP 95 11 3021.0
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLMWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLMWIGIYHSGNTYNNPSL 63
QY 62 KSRVTVSVDTSKNHFSLRLSSVTAADTAAYYCAR--SDGYTLDMWGCGTLTVTVSS 114
DB 64 KSRVTVSVDTSKNHFSLRLSSVTAADTAAYYCAR--SDGYTLTVSS 119

RESULT 8

US-09-490-070A-39
Sequence 39, Application US/09490070A

Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3,6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;
QY 2 ESGGGLVKPSQTLSTCTVSGSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYNPBL 61
DB 6 ESGGGLVKPSQTLSTCTVSGSGSIS--YYWSWIRQPPKGLGEMIGYIYSGSTNNPBL 63
QY 62 KSRVTMSVPTSKNHFSLRLSVTAADTAAYYYCAR--SDG--YTLDMNGOGTLVTSS 114
DB 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYYYCARWGSDGFYAMDYWGOGTLVTSS 119
RESULT 9
US-09-490-070A-65
Sequence 65, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
ADDRESSEE: Knappik, Achim
APPLICANT: Knappik, Achim
Packer, Peter
Ilag, Vic
Ge, Liming
Moreney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65
Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3,6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;
QY 2 ESGGGLVKPSQTLSTCTVSGSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYNPBL 61
DB 6 ESGGGLVKPSQTLSTCTVSGSGSIS--YYWSWIRQPPKGLGEMIGYIYSGSTNNPBL 63
QY 62 KSRVTMSVPTSKNHFSLRLSVTAADTAAYYYCAR--SDG--YTLDMNGOGTLVTSS 114
DB 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYYYCARWGSDGFYAMDYWGOGTLVTSS 119
RESULT 10
US-09-490-153-39
Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
ADDRESSEE: Knappik, Achim
APPLICANT: Knappik, Achim
Packer, Peter
Ilag, Vic
Ge, Liming
Moreney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-153-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSSETLSTCTVSGGSISS--YVMSWIRPPGKGLWIGIYHSGNTYYNPSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDG-YTLDMNGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVSS 119

RESULT 11
US-09-490-153-65
Sequence 65, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSSETLSTCTVSGGSISS--YVMSWIRPPGKGLWIGIYHSGNTYYNPSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDG-YTLDMNGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVSS 119

RESULT 12
US-09-490-324-39
Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSSETLSTCTVSGGSISS--YVMSWIRPPGKGLWIGIYHSGNTYYNPSL 63

Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYMSWIRQPKGLEWIGIYYSGSTNNPSL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCAR--SDG-YTLDNMGQGLVTYVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYCARMGDGFYAMDYMGQGLVTYVSS 119

RESULT 13
US-09-490-324-65
; Sequence 65, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 3.6e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSETLSLTCTVSGGSISSGYWMSWIRQPKGLEWIGIYYSGSTNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYMSWIRQPKGLEWIGIYYSGSTNNPSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCAR--SDG-YTLDNMGQGLVTYVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYCARMGDGFYAMDYMGQGLVTYVSS 119

RESULT 14
US-10-330-613A-25
; Sequence 25, Application US/10330613A
; Patent No. 6924360

; GENERAL INFORMATION:
; APPLICANT: Guada, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRP
; ORGANISM: Homo Sapiens
US-10-330-613A-25

Query Match 81.0%; Score 497.5; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 1.2e-42;
Matches 95; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSETLSLTCTVSGGSISSGYWMSWIRQPKGLEWIGIYYSGSTNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGSISSGYWMSWIRQPKGLEWIGIYYSGSTNNPSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCAR--DGYTLDNMGQGLVTYVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSMTAADTAIVYCARBRETAGFDYMGQGLVTYVSS 119

RESULT 15
US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match 80.8%; Score 496; DB 1; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPQSTLSLTCTVSGSGSIRSGYYWMIROPKGLKLEWIGYIYHSGNTYYNPSL 61
DB 6 ESGPGLVKPQSTLSLTCTVSGSGSIRSGYYWMIROPKGLKLEWIGYIYHSGNTYYNPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSD---GYTLDMWGQGLVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARSGYGYGMDWGQGLVTVSS 122

Search completed: August 30, 2006, 00:37:09
Job time: 16.5455 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 65.2909 Seconds
(Without alignments)
808.788 Million cell updates/sec

Title: US-10-027-725A-9

Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLTVTSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	US-10-027-725A-9	Sequence 9, Appl1
2	600	97.7	114	US-10-027-725A-8	Sequence 8, Appl1
3	556	90.6	114	US-10-027-725A-7	Sequence 7, Appl1
4	524.5	85.4	121	US-10-309-762-152	Sequence 152, App
5	524	85.3	118	US-10-309-762-138	Sequence 138, App
6	523.5	85.3	123	US-10-309-762-10	Sequence 10, Appl
7	521	84.9	120	US-10-309-762-13	Sequence 13, Appl
8	521	84.9	120	US-10-309-762-144	Sequence 144, App
9	521	84.9	122	US-10-309-762-147	Sequence 147, App
10	520	84.7	121	US-09-972-656-80	Sequence 80, Appl
11	519.5	84.6	121	US-10-309-762-151	Sequence 151, App
12	519.5	84.6	125	US-10-309-762-11	Sequence 11, Appl
13	518	84.4	121	US-10-805-177-56	Sequence 56, Appl
14	517.5	84.3	119	US-10-309-762-140	Sequence 140, App
15	517.5	84.3	148	US-11-131-648-13	Sequence 13, Appl
16	517.5	84.3	148	US-11-131-648-35	Sequence 35, Appl
17	517	84.2	125	US-10-805-177-53	Sequence 53, Appl
18	516.5	84.1	123	US-10-309-762-12	Sequence 12, Appl
19	516.5	84.1	144	US-10-893-576-35	Sequence 35, Appl
20	516	84.0	124	US-10-309-762-75	Sequence 75, Appl
21	515.5	84.0	143	US-10-309-762-96	Sequence 96, Appl
22	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
23	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
24	515.5	84.0	117	US-10-660-357-13	Sequence 13, Appl
25	514	83.7	120	US-10-309-762-128	Sequence 128, App
26	514	83.7	120	US-10-309-762-139	Sequence 139, App
27	514	83.7	121	US-10-308-817-137	Sequence 137, App

28	514	83.7	121	US-10-453-698-137	Sequence 137, App
29	514	83.7	122	US-10-984-960A-56	Sequence 56, Appl
30	513	83.6	116	US-10-309-762-127	Sequence 127, App
31	512.5	83.5	125	US-10-309-762-8	Sequence 8, Appl1
32	512.5	83.5	125	US-10-309-762-16	Sequence 16, Appl
33	512.5	83.5	480	US-10-910-901-6	Sequence 6, Appl1
34	511.5	83.3	119	US-10-309-762-131	Sequence 131, App
35	511.5	83.3	140	US-10-893-576-41	Sequence 41, Appl
36	511	83.2	110	US-10-309-762-74	Sequence 74, Appl
37	510.5	83.1	123	US-10-309-762-9	Sequence 9, Appl1
38	510.5	83.1	127	US-10-309-762-14	Sequence 14, Appl
39	510.5	83.1	148	US-10-893-576-31	Sequence 31, Appl
40	509	82.9	149	US-10-910-901-22	Sequence 22, Appl
41	508.5	82.8	123	US-10-893-576-190	Sequence 190, App
42	508.5	82.8	125	US-10-309-762-153	Sequence 153, App
43	508	82.7	128	US-10-727-155-2	Sequence 2, Appl1
44	508	82.7	128	US-10-727-155-10	Sequence 10, Appl
45	508	82.7	128	US-10-727-155-30	Sequence 30, Appl

ALIGNMENTS

```
RESULT 1
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-9

Query Match      100.0%; Score 614; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LBSGPGLVKPSQTLSTCTVSGGSIRSGGYWMIROPGKGLWIGYIYHSGNTYVNS 60
      |||||
DB      1 LBSGPGLVKPSQTLSTCTVSGGSIRSGGYWMIROPGKGLWIGYIYHSGNTYVNS 60
      |||||

QY      61 LKSRVTMSVDTSKNHFSLLSSVTADTVYTCARSDGYTLDMWGQGLTVTSS 114
      |||||
DB      61 LKSRVTMSVDTSKNHFSLLSSVTADTVYTCARSDGYTLDMWGQGLTVTSS 114
      |||||

RESULT 2
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
```

ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match 97.7%; Score 600; DB 4; Length 114;
Best Local Similarity 96.5%; Pred. No. 2,4e-46;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPS 60
DB 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLTVVSS 114
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLTVVSS 114

RESULT 3
US-10-027-725A-7

Sequence 7, Application US/10027725A
Publication No. US20030082659A1

GENERAL INFORMATION:
APPLICANT: Flicker, Sabine
TITLE OF INVENTION: Group 2 Allergen Specific IGB-fabs and Use Thereof
FILE REFERENCE: 25401-4
CURRENT APPLICATION NUMBER: US/10/027,725A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/259,436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match 90.6%; Score 556; DB 4; Length 114;
Best Local Similarity 90.4%; Pred. No. 2,2e-42;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPS 60
DB 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLTVVSS 114
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLTVVSS 114

RESULT 4

US-10-309-762-152
Sequence 152, Application US/10309762
Publication No. US20040018198A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 152
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-152

Query Match 85.4%; Score 524.5; DB 4; Length 121;
Best Local Similarity 86.2%; Pred. No. 1,6e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSD---GYTLDMNGGTLTVVSS 114
DB 66 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDYTLDMNGGTLTVVSS 121

RESULT 5
US-10-309-762-138

Sequence 138, Application US/10309762
Publication No. US20040018198A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-138

Query Match 85.3%; Score 524; DB 4; Length 118;
Best Local Similarity 88.5%; Pred. No. 1,7e-39;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFWIGIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLTVVSS 114
DB 66 KSRVTMSVDTSKNHFSLRLSSVTAADTAAYVYCARSDGYTLDMNGGTLTVVSS 118

RESULT 6

US-10-309-762-10
Sequence 10, Application US/10309762
Publication No. US20040018198A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: AGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-10

US-10-309-762-152

US-10-309-762-10

Query Match 85.3%; Score 523.5; DB 4; Length 123;
Best Local Similarity 85.6%; Pred. No. 2e-39;
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 65
QY 62 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--DGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--DGYTLDNWGQGLTVTVSS 123

RESULT 7

US-10-309-762-13
Sequence 13, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Folitz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-13

Query Match 84.9%; Score 521; DB 4; Length 120;
Best Local Similarity 87.1%; Pred. No. 3.2e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 65
QY 62 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--DGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--DGYTLDNWGQGLTVTVSS 120

RESULT 8

US-10-309-762-144
Sequence 144, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Folitz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 144
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens

US-10-309-762-144

Query Match 84.9%; Score 521; DB 4; Length 120;
Best Local Similarity 87.1%; Pred. No. 3.2e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 65
QY 62 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--DGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--DGYTLDNWGQGLTVTVSS 120

RESULT 9

US-10-309-762-147
Sequence 147, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Folitz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 147
LENGTH: 122
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-147

Query Match 84.9%; Score 521; DB 4; Length 122;
Best Local Similarity 85.5%; Pred. No. 3.3e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLMIGIYHSGNTYNNPSL 65
QY 62 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--SDGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNPFSLRLSSVTAADTAAYYCAR--SDGYTLDNWGQGLTVTVSS 122

RESULT 10

US-09-972-656-80
Sequence 80, Application US/09972656
Publication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT: Deebhande, Rajendra
APPLICANT: Tsai, Wei-Wei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 80
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-80

Query Match 84.7%; Score 520; DB 3; Length 221;

Best Local Similarity 86.7%; Pred. No. 7.3e-39;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
Db 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 118

RESULT 11

US-10-309-762-151
Sequence 151, Application US/10309762
Publication No. US20040018196A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean

APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275

PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151

LENGTH: 121
TYPE: PRT

ORGANISM: Homo sapiens
US-10-309-762-151

Query Match 84.6%; Score 519.5; DB 4; Length 121;
Best Local Similarity 86.2%; Pred. No. 4.4e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
Db 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 121

RESULT 12

US-10-309-762-11
Sequence 11, Application US/10309762
Publication No. US20040018196A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean

APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275

PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11

LENGTH: 125
TYPE: PRT

ORGANISM: Homo sapiens
US-10-309-762-11

Query Match 84.6%; Score 519.5; DB 4; Length 125;
Best Local Similarity 83.3%; Pred. No. 4.6e-39;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;

QY 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
Db 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 125

RESULT 13

US-10-805-177-56
Sequence 56, Application US/10805177
Publication No. US2005008449A1

GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.

APPLICANT: Chen, Francine
APPLICANT: Bezabeh, Blinam

APPLICANT: Foltz, Ian
APPLICANT: Tse, Kam Fai

APPLICANT: Jeffers, Michael
APPLICANT: Mesiri, Mehdi

APPLICANT: Starling, Gary
APPLICANT: Mezes, Peter

APPLICANT: Khramtsov, Nikolai
TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN

FILE REFERENCE: ABXCUR.006A
CURRENT APPLICATION NUMBER: US/10/805,177

CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: 60/456,652

PRIOR FILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 141

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56

LENGTH: 121
TYPE: PRT

ORGANISM: Homo Sapiens
US-10-805-177-56

Query Match 84.4%; Score 518; DB 5; Length 121;
Best Local Similarity 84.3%; Pred. No. 6.1e-39;
Matches 97; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

QY 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61
Db 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 120

RESULT 14

US-10-309-762-140
Sequence 140, Application US/10309762
Publication No. US20040018196A1

GENERAL INFORMATION:
APPLICANT: Gudas, Jean

APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762

CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275

PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-140

Query Match 84.3%; Score 517.5; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 6,6e-39;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 65

QY 62 KSRVTWSVDTSKNHFSLRLSSVTAADTAVYYCARSD-GYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARGNYYGMDVWGQGLTVTVSS 119

RESULT 15

US-11-131-648-13
; Sequence 13, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO BSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-13

Query Match 84.3%; Score 517.5; DB 6; Length 148;
Best Local Similarity 83.5%; Pred. No. 8.2e-39;
Matches 101; Conservative 4; Mismatches 7; Indels 9; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 61
Db 15 ESGPGLVKPSQTLSTCTVSGGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 74

QY 62 KSRVTWSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTVSS 113
Db 75 KSRVTWSVDTSKNQFSLKLSSTVTAADTAVYYCAR-DEITMIRGYYGMDVWGQGLTVTVSS 133

QY 114 S 114
Db 134 S 134

Search completed: August 30, 2006, 00:50:38
Job time : 66.2909 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 13.4727 Seconds
(without alignments)

578.960 Million cell updates/sec

Title: US-10-027-725a-9

Perfect score: 614

Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_NEW_PUB.dep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US06_NEW_PUB.dep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_NEW_PUB.dep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_NEW_PUB.dep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/PCT_NEW_PUB.dep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_NEW_PUB.dep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_NEW_PUB.dep:*
- 8: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US60_NEW_PUB.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	85.4	118	6	US-10-981-300-51 Sequence 51, App1
2	502.5	81.8	119	7	US-11-304-986-25 Sequence 25, App1
3	501.5	81.7	149	7	US-11-355-464-13 Sequence 13, App1
4	501.5	81.7	149	7	US-11-355-464-16 Sequence 16, App1
5	497.5	81.0	121	7	US-11-337-300-84 Sequence 84, App1
6	497.5	81.0	248	7	US-11-337-300-94 Sequence 94, App1
7	495.5	80.7	121	7	US-11-211-917-82 Sequence 82, App1
8	495.5	80.7	466	7	US-11-211-917-86 Sequence 86, App1
9	493.5	80.4	121	7	US-11-211-917-98 Sequence 98, App1
10	493.5	80.4	466	7	US-11-211-917-70 Sequence 70, App1
11	492	80.1	118	7	US-11-211-917-109 Sequence 109, App1
12	492	80.1	118	7	US-11-211-917-109 Sequence 109, App1
13	492	80.1	120	7	US-11-211-917-142 Sequence 142, App1
14	491.5	80.0	121	7	US-11-211-917-66 Sequence 66, App1
15	490.5	79.9	118	6	US-10-981-300-52 Sequence 52, App1
16	490.5	79.9	180	6	US-10-981-300-4 Sequence 4, App1
17	489	79.6	115	6	US-10-981-300-53 Sequence 53, App1
18	489	79.6	126	6	US-10-994-679-68 Sequence 68, App1
19	485.5	79.1	121	7	US-11-211-917-26 Sequence 26, App1
20	485.5	79.1	466	7	US-11-211-917-30 Sequence 30, App1
21	483	78.7	108	7	US-11-281-266-82 Sequence 82, App1
22	479.5	78.1	107	6	US-10-484-105-18 Sequence 18, App1
23	476.5	77.6	118	6	US-10-981-300-54 Sequence 54, App1
24	476.5	77.6	443	6	US-10-981-300-20 Sequence 20, App1
25	476	77.5	120	7	US-11-211-917-108 Sequence 108, App1

26	474.5	77.3	113	7	US-11-290-687-17 Sequence 17, App1
27	474	77.2	247	6	US-10-539-402-10 Sequence 10, App1
28	473.5	77.1	119	7	US-11-211-917-18 Sequence 18, App1
29	473.5	77.1	464	7	US-11-211-917-22 Sequence 22, App1
30	472	76.9	244	7	US-11-402-010-77 Sequence 77, App1
31	471.5	76.8	121	6	US-10-994-679-60 Sequence 60, App1
32	468	76.2	108	7	US-11-281-266-85 Sequence 85, App1
33	467	76.1	286	7	US-11-154-103-8 Sequence 8, App1
34	465	75.7	444	7	US-11-317-786B-17 Sequence 17, App1
35	465	75.7	248	7	US-11-317-786B-9 Sequence 9, App1
36	461.5	75.2	197	1	US-09-784-950-25 Sequence 25, App1
37	459.5	74.8	117	7	US-11-290-687-41 Sequence 41, App1
38	459.5	74.8	127	7	US-11-259-133-202 Sequence 202, App1
39	458	74.6	124	7	US-11-111-688-1 Sequence 1, App1
40	458	74.6	126	7	US-11-111-688-55 Sequence 55, App1
41	458	74.6	244	7	US-11-317-786B-19 Sequence 19, App1
42	458	74.6	448	7	US-11-317-786B-11 Sequence 11, App1
43	457	74.4	240	7	US-11-317-786B-15 Sequence 15, App1
44	457	74.4	445	7	US-11-317-786B-32 Sequence 32, App1
45	457	74.4	448	7	US-11-317-786B-7 Sequence 7, App1

ALIGNMENTS

```
RESULT 1
US-10-981-300-51
; Sequence 51, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-300-51

Query Match      85.4%; Score 524.5; DB 6; Length 118;
Best Local Similarity 88.5%; Pred. No. 1.4e-39;
Matches 100; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY      2  ESGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPGKGLWIGYVHSGNTYNNPSL 61
DB      6  ESGPGLVKPSQTLSTCTVSGSISGYYWMIROPGKGLWIGYVHSGNTYNNPSL 65

QY      62 KSRVTSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
DB      66 KSRVTSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 117

RESULT 2
US-11-304-986-25
; Sequence 25, Application US/11304986
; Publication No. US20060165682A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth and Neirajab et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; FILE REFERENCE: ELN-055
; CURRENT APPLICATION NUMBER: US/11/304,986
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: 60/636684
; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
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```
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct, consensus sequence for heavy chain
; OTHER INFORMATION: framework region
US-11-304-986-25
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Query Match      81.8%; Score 502.5; DB 7; Length 119;
Best Local Similarity 85.3%; Pred. No. 1.3e-37;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;
```

```
QY 2 EESGGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 EESGGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYVNSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCAR--SDG-YTLDNMGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTISVDTSKNQPFLKLSSTVTAADTAVYYCARMGDGFYAMDYWGQGLTVTVSS 119
```

```
RESULT 3
US-11-355-464-13
; Sequence 13, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: CHALILITA-EID, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT FILING DATE: 2006-02-15
; PRIOR FILING DATE: 2005-05-17
; PRIOR FILING DATE: 2004-12-02
; PRIOR FILING DATE: 2004-10-21
; PRIOR FILING DATE: 2004-10-12
; PRIOR FILING DATE: 2004-10-05
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-355-464-13
```

```
Query Match      81.7%; Score 501.5; DB 7; Length 149;
Best Local Similarity 81.8%; Pred. No. 1.9e-37;
Matches 99; Conservative 5; Mismatches 8; Indels 9; Gaps 2;
```

```
QY 2 EESGGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 EESGGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYVNSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGTYT-----LDNMGQGLTVTVS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTISVDTSKNQPFLKLSSTVTAADTAVYYCAR-DHITWVRGVKMDYWGQGLTVTVS 122
```

```
QY 114 S 114
Db 123 S 123
```

```
RESULT 4
US-11-355-464-16
; Sequence 16, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: CHALILITA-EID, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT FILING DATE: 2006-02-15
; PRIOR FILING DATE: 2005-05-17
; PRIOR FILING DATE: 2004-12-02
; PRIOR FILING DATE: 2004-10-21
; PRIOR FILING DATE: 2004-10-12
; PRIOR FILING DATE: 2004-10-05
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-355-464-16
```

```
Query Match      81.7%; Score 501.5; DB 7; Length 149;
Best Local Similarity 81.8%; Pred. No. 1.9e-37;
Matches 99; Conservative 5; Mismatches 8; Indels 9; Gaps 2;
```

```
QY 2 EESGGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 EESGGLVPSQTLSTLTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYVNSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGTYT-----LDNMGQGLTVTVS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTISVDTSKNQPFLKLSSTVTAADTAVYYCAR-DHITWVRGVKMDYWGQGLTVTVS 122
```

```
QY 114 S 114
Db 123 S 123
```

```
RESULT 5
US-11-337-300-84
; Sequence 84, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Cruceil Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruijf, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmilt, Jaap
```

;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
;; FILE REFERENCE: 0091 WO 00 ORD
;; CURRENT APPLICATION NUMBER: US/11/337,300
;; CURRENT FILING DATE: 2006-01-20
;; NUMBER OF SEQ ID NOS: 478
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 84
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Variable heavy chain of SC03-017
US-11-337-300-84

Query Match 81.0%; Score 497.5; DB 7; Length 121;
Best Local Similarity 83.5%; Pred. No. 3.5e-37;
Matches 96; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 2 ESGPGLVKPESQTLSTCTVSGGSIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61
DB 8 ESGAGLKPSETSLTCTVSGGSVSSGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 67
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCA--RSDGYTLDNWGGTLVTYSS 114
DB 68 KSRVTISVDTSKQFSLKLSSTVTAADTAIVYCAKRSRAGF-FDYWGQGTIVTYSS 121

RESULT 6
US-11-337-300-94
;; Sequence 94, Application US/11337300
;; Publication No. US20060121580A1
;; GENERAL INFORMATION:
;; APPLICANT: Crucell Holland B.V.
;; APPLICANT: ter Meulen, Jan H.
;; APPLICANT: De Kruif, Cornelis A.
;; APPLICANT: van den Brink, Edward N.
;; APPLICANT: Goudemil, Jaap
;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
;; FILE REFERENCE: 0091 WO 00 ORD
;; CURRENT APPLICATION NUMBER: US/11/337,300
;; CURRENT FILING DATE: 2006-01-20
;; NUMBER OF SEQ ID NOS: 478
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 94
;; LENGTH: 248
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: SC03-017
US-11-337-300-94

Query Match 81.0%; Score 497.5; DB 7; Length 248;
Best Local Similarity 83.5%; Pred. No. 7e-37;
Matches 96; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 2 ESGPGLVKPESQTLSTCTVSGGSIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61
DB 9 ESGAGLKPSETSLTCTVSGGSVSSGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 68
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCA--RSDGYTLDNWGGTLVTYSS 114
DB 69 KSRVTISVDTSKQFSLKLSSTVTAADTAIVYCAKRSRAGF-FDYWGQGTIVTYSS 122

RESULT 7
US-11-211-917-82
;; Sequence 82, Application US/11211917
;; Publication No. US20060093600A1
;; GENERAL INFORMATION:
;; APPLICANT: BEDIAN, VAHE
;; APPLICANT: GLADUE, RONALD P.
;; APPLICANT: CORVALAN, JOSE
;; APPLICANT: JIA, XIAO-CHI

;; APPLICANT: FENG, XIAO
;; TITLE OF INVENTION: ANTIBODIES TO CD40
;; FILE REFERENCE: ABX-PP/3 US
;; CURRENT APPLICATION NUMBER: US/11/211,917
;; CURRENT FILING DATE: 2005-08-25
;; PRIOR APPLICATION NUMBER: US/10/292,088
;; PRIOR FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 60/348,980
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 82
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-211-917-82

Query Match 80.7%; Score 495.5; DB 7; Length 121;
Best Local Similarity 83.1%; Pred. No. 5.3e-37;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPESQTLSTCTVSGGSIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61
DB 6 ESGGGLVKPSETSLTCTVSGGSIR--GYWSWIRPPGKGLWIGIYHSGNTYNPSTL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCA--RSDGYTLDNWGGTLVTYSS 114
DB 64 KSRVTISVDTSKQFSLKLSSTVTAADTAIVYCAKRSRAGF-FDYWGQGTIVTYSS 121

RESULT 8
US-11-211-917-86
;; Sequence 86, Application US/11211917
;; Publication No. US20060093600A1
;; GENERAL INFORMATION:
;; APPLICANT: BEDIAN, VAHE
;; APPLICANT: GLADUE, RONALD P.
;; APPLICANT: CORVALAN, JOSE
;; APPLICANT: JIA, XIAO-CHI
;; APPLICANT: FENG, XIAO
;; TITLE OF INVENTION: ANTIBODIES TO CD40
;; FILE REFERENCE: ABX-PP/3 US
;; CURRENT APPLICATION NUMBER: US/11/211,917
;; CURRENT FILING DATE: 2005-08-25
;; PRIOR APPLICATION NUMBER: US/10/292,088
;; PRIOR FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 60/348,980
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 86
;; LENGTH: 466
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-211-917-86

Query Match 80.7%; Score 495.5; DB 7; Length 466;
Best Local Similarity 83.1%; Pred. No. 1.9e-36;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPESQTLSTCTVSGGSIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61
DB 25 ESGGGLVKPSETSLTCTVSGGSIR--GYWSWIRPPGKGLWIGIYHSGNTYNPSTL 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAIVYCA--RSDGYTLDNWGGTLVTYSS 114
DB 83 KSRVTISVDTSKQFSLKLSSTVTAADTAIVYCAKRSRAGF-FDYWGQGTIVTYSS 140

RESULT 9
US-11-211-917-98
;; Sequence 98, Application US/11211917
;; Publication No. US20060093600A1

```

; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-98

Query Match      80.4%; Score 493.5; DB 7; Length 121;
Best Local Similarity 82.2%; Pred. No. 7.9e-37;
Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;
```

```

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 61
DB 6 ESGPGLVKPSETLSTCTVSGSIR--GYWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYYCARSDGYTLDD-----NMGGCTLVTVSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTADTAIVYYCARKGLYGDYGFAPMGOGTLTVTVSS 121
```

```

RESULT 10
US-11-211-917-70
; Sequence 70, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-70
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```

Query Match      80.4%; Score 493.5; DB 7; Length 466;
Best Local Similarity 82.2%; Pred. No. 2.9e-36;
Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;
```

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 61
DB 25 ESGPGLVKPSETLSTCTVSGSIR--GYWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 82
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYYCARSDGYTLDD-----NMGGCTLVTVSS 114
DB 83 KSRVTISVDTSKNQFSLKLSVTADTAIVYYCARKGLYGDYGFAPMGOGTLTVTVSS 140

```

RESULT 11
US-11-211-917-109
; Sequence 109, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-109

Query Match      80.1%; Score 492; DB 7; Length 118;
Best Local Similarity 84.3%; Pred. No. 1.1e-36;
Matches 97; Conservative 5; Mismatches 9; Indels 4; Gaps 2;
```

```

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 61
DB 6 ESGPGLVKPSETLSTCTVSGSIRSS--YWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYYCARSDGYT--LDNMGGCTLVTVSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTADTAIVYYCARDYGDGNSYFDYMGOGTLTVTVSS 118
```

```

RESULT 12
US-11-211-917-142
; Sequence 142, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-142
```

```

Query Match      80.1%; Score 492; DB 7; Length 118;
Best Local Similarity 85.2%; Pred. No. 1.1e-36;
Matches 98; Conservative 5; Mismatches 8; Indels 4; Gaps 3;
```

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 61
DB 6 ESGPGLVKPSETLSTCTVSGSIRSS--YWMSWIRPPGKGLMWIGIYHSGNTYNPSTL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARSDGIDYVWFPWPGGGLVTYSS 118

RESULT 13

US-11-281-266-6
Sequence 6, Application US/11281266
Publication No. US20060140948A1
GENERAL INFORMATION:

APPLICANT: Foltz, Ian
APPLICANT: Fagioni, Raffaella
APPLICANT: Senaldi, Giorgio
APPLICANT: Manchulenko, Kathy
APPLICANT: Kang, Jaespal
APPLICANT: Rathnaswami, Palaniswami
APPLICANT: Anilwalia, Kiran
APPLICANT: Ford, Orlit
APPLICANT: Klakamp, Scott
TITLE OF INVENTION: FULLY HUMAN MONOCLONAL ANTIBODIES TO
TITLE OF INVENTION: II-13
FILE REFERENCE: ABGENIX.119A
CURRENT APPLICATION NUMBER: US/11/281,266
CURRENT FILING DATE: 2005-11-16
PRIOR APPLICATION NUMBER: 60/629,135
PRIOR FILING DATE: 2004-11-17
PRIOR APPLICATION NUMBER: 60/728,604
PRIOR FILING DATE: 2005-10-19
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens

US-11-281-266-6

Query Match 80.1%; Score 492; DB 7; Length 120;
Best Local Similarity 81.2%; Pred. No. 1,1e-36;
Matches 95; Conservative 8; Mismatches 8; Indels 6; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIR--YYMSWIRQPPGKGLWIGIYHSGNTYNNPSL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARSDGIDYVWFPWPGGGLVTYSS 120

RESULT 14

US-11-211-917-66
Sequence 66, Application US/11211917
Publication No. US20060093600A1
GENERAL INFORMATION:

APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JTA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR APPLICATION NUMBER: US/10/292,088
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/348,380
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 66
LENGTH: 121
TYPE: PRT

ORGANISM: Homo sapiens
US-11-211-917-66

Query Match 80.0%; Score 491.5; DB 7; Length 121;
Best Local Similarity 82.2%; Pred. No. 1.2e-36;
Matches 97; Conservative 5; Mismatches 9; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIR--GYWMSWIRQPPGKGLWIGIYHSGNTYNNPSL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARSDGIDYVWFPWPGGGLVTYSS 121

RESULT 15

US-10-981-300-52
Sequence 52, Application US/10981300
Publication No. US20060093599A1
GENERAL INFORMATION:

APPLICANT: GADIT GAZIT-BORNSTEIN
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
TITLE OF INVENTION: FOR MAKING AND USING THE SAME
FILE REFERENCE: ABGX-005
CURRENT APPLICATION NUMBER: US/10/981,300
CURRENT FILING DATE: 2004-11-03
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens

US-10-981-300-52

Query Match 79.9%; Score 490.5; DB 6; Length 118;
Best Local Similarity 82.3%; Pred. No. 1.4e-36;
Matches 93; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLVTYSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARSDG-YT-LDNGGGLVTYSS 117

Search completed: August 30, 2006, 00:52:02
Job time: 14.4727 secs

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PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IGG comprising
 PT variable region of group 2 allergen specific-human IGE Fabs; useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 39; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IGE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IGE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific Fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The Fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific Fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IGE antibodies to Phi p 2. The present sequence represents the human IGE
 CC Fab, clone 94 light chain protein of the invention

XX Sequence 106 AA;

Query Match 98.2%; Score 533; DB 5; Length 106;
 Best Local Similarity 99.1%; Pred. No. 5.6e-33;
 Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
 Db 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60

QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASTFGQGTVEIKR 106
 Db 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASTFGQGTVEIKR 106

RESULT 2
 AAR54260
 ID AAR54260 standard; protein; 107 AA.

XX AAR54260;
 AC
 DT 25-MAR-2003 (revised)
 DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b22.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KM neutralisation; monoclonal antibody; kappa light chain; variable region;
 KM framework; complementarity determining region.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..21
 FT /label= FR1
 FT Region
 FT 22..33
 FT /label= CDR1
 FT Region
 FT 34..48
 FT /label= FR2
 FT Region
 FT 49..55
 FT /label= CDR2
 FT Region
 FT 56..87
 FT /label= FR3
 FT Region
 FT 88..95
 FT /label= CDR3
 FT 96..107
 FT /label= FR4
 FT Region
 XX MO9407922-A1.

PD 14-APR-1994.

XX 30-SEP-1993; 93MO-US009328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI) SCRIPPS RES INST.

PI Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with gp120 or
 PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
 PT diagnosis and for passive immuno-therapy.

XX Claim 5; Page 189; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
 CC using primers specific for heavy and light chain variable regions. The
 CC amplification products were inserted into a disclonon vector to produce
 CC a library of fragments. E.coli XL1 Blue cells were transformed with the
 CC library. Filamentous phage were produced which expressed the MAb regions
 CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
 CC immunoreactive clones. The light chain VK region sequence AAR54260
 CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 107 AA;

Query Match 87.5%; Score 475; DB 2; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.4e-28;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
 Db 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60

QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASTFGQGTVEIKR 106
 Db 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASTFGQGTVEIKR 106

RESULT 3
 AAM01283
 ID AAM01283 standard; protein; 107 AA.

XX AAM01283;

XX 29-JAN-1997 (first entry)

XX VL region of HIV neutralising MAb, clone b22 and B35.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
 KM HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KM virus infectivity assay; precursor gp160; immunocompetence; human;
 KM anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..21
 FT /label= FR1
 FT Region
 FT 22..32
 FT /label= CDR1
 FT Region
 FT 33..47
 FT /label= FR2
 FT Region
 FT 48..54
 FT /label= CDR2
 FT Region
 FT 55..86
 FT /label= FR3
 FT Region
 FT 87..95
 FT /label= CDR3
 FT 96..107
 FT /label= CDR3
 FT Region

FT /label= FR4
 XX MO9602273-A1.
 XX 01-FEB-1996.
 XX 11-JUL-1995; 95WO-US008743.
 XX 18-JUL-1994; 94US-00276852.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX MPI, 1996-179601/18.
 XX Monoclonal antibody binding to VI/12 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.
 XX Example; Fig 11; 366pp; English.
 XX The sequences given in AA01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JH2 gene
 CC clones, b22 and B35. A Mab containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by
 CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds
 CC mature gp120 preferentially over the precursor gp160. The Mab may be used
 CC for determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection
 XX SO Sequence 107 AA;
 XX
 XX Query Match 87.5%; Score 475; DB 2; Length 107;
 XX Best Local Similarity 87.7%; Pred. No. 1.4e-28;
 XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 XX
 XX 1 ELTQSPSSISASVGDVVTISCRASORINTYLMNYQHKGKAPKLLIYAASSLSQGVPSRF 60
 XX 1 ELTQSPSSISASVGDVVTITCRASQSISSYLMNYQKPGKAPKLLIYAASSLSQGVPSRF 60
 XX
 XX 61 SSGSGYGTDFLTITSSIQPEDFASYCOESLSASYTFGCGTKVEIKR 106
 XX 61 SSGSGGTDFLTITSSIQPEDFATYYCOQSYSTPYTFGCGTKLEIKR 106
 XX
 XX RESULT 4
 XX AA98244
 XX ID AA98244 standard; protein; 107 AA.
 XX AC AA98244;
 XX
 XX 04-JUL-2000 (first entry)
 XX Anti-gp120 antibody light chain variable region from clone b22.
 XX
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
 XX passive immuno:therapy; reduce severity; HIV-induced disease;
 XX immunocompetence; active immunisation.
 XX Homo sapiens.
 XX AU9848754-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048754.
 XX 16-SEP-1999; 99AU-00048754.
 XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;
 XX MPI, 2000-246867/22.
 XX Human neutralising monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 XX glycoprotein-120.
 XX Example 9; Fig 11; 374pp; English.
 XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AA98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 XX derivation
 XX SO Sequence 107 AA;
 XX
 XX Query Match 87.5%; Score 475; DB 3; Length 107;
 XX Best Local Similarity 87.7%; Pred. No. 1.4e-28;
 XX Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 XX
 XX 1 ELTQSPSSISASVGDVVTISCRASORINTYLMNYQHKGKAPKLLIYAASSLSQGVPSRF 60
 XX 1 ELTQSPSSISASVGDVVTITCRASQSISSYLMNYQKPGKAPKLLIYAASSLSQGVPSRF 60
 XX
 XX 61 SSGSGYGTDFLTITSSIQPEDFASYCOESLSASYTFGCGTKVEIKR 106
 XX 61 SSGSGGTDFLTITSSIQPEDFATYYCOQSYSTPYTFGCGTKLEIKR 106
 XX
 XX RESULT 5
 XX AA95135
 XX ID AA95135 standard; protein; 107 AA.
 XX AC AA95135;
 XX
 XX 30-JUN-2000 (first entry)
 XX Anti-gp120 antibody light chain variable region from clone b22.
 XX
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX Homo sapiens.

```

XX
PN AU9948756-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX
PA (SCRI ) SCRIAPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-293393/26.
XX
PT Novel human monoclonal antibodies which immunoreact with and neutralize
XX human immunodeficiency virus useful for treating HIV infections.
XX
PS Example 9; Fig 11; 366pp; English.
XX
CC The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
XX
SQ Sequence 107 AA;
XX
Query Match 87.5%; Score 475; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNYYQHKRGKAPKLLIYAASSLGVSRSR 60
DB 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNYYQHKRGKAPKLLIYAASSLGVSRSR 60
XX
QY 61 SGGSGYGDPTLTSSLOFEDPASYYCOESLSASTYFCGKTVEIKR 106
DB 61 SGGSGYGDPTLTSSLOFEDPASYYCOESLSASTYFCGKTVEIKR 106
XX
RESULT 6
AEF65392
ID AEF65392 standard; protein; 214 AA.
XX
AC AEF65392;
XX
DT 06-APR-2006 (first entry)
XX
DE Anti-Rhd Fab clone Rhd200.164G10 Lc region sequence.
XX
KW antibody engineering; anti-Rhesus D antibody; anti-Rhd antibody;

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```

KW Gene expression; hemostatic; therapeutic; newborn hemolytic disease;
KM thrombocytopenic purpura; TRP; antibody.
XX
XX Homo sapiens.
XX
PN WO2006007850-A1.
XX
PD 26-JAN-2006.
XX
PF 18-JUL-2005; 2005WO-DK000501.
XX
PR 20-JUL-2004; 2004DK-00001133.
XX
PR 22-DEC-2004; 2004DK-00001992.
XX
PA (SYMP-) SYMPHOGEN AS.
XX
PI Rasmussen SK, Tolstrup AB, Frederiksen SB, Haurum J;
XX
DR WPI; 2006-110334/11.
XX
DR N-PSDB; AEF65280.
XX
PT Generating a collection of cells for expression of anti-Rhesus D
PT recombinant polyclonal antibodies, involves selecting cells having
PT integrated copy of antibody-encoding nucleic acid from library of anti-
PT Rhd antibody expression vectors.
XX
PS Example 1; SEQ ID NO 221; 245pp; English.
XX
XX The invention relates to generating (M1) a collection of cells suitable
XX as manufacturing cell line for expression of anti-Rhesus D (Rhd)
XX recombinant polyclonal antibody. The method involves introducing a
XX library of anti-Rhd antibody expression vectors into a host cell line,
XX and selecting cells comprising an integrated copy of the anti-Rhd
XX antibody-encoding nucleic acid segment from the library of anti-Rhd
XX antibody expression vectors, where each individual vector of library
XX comprises one single copy of a nucleic acid segment encoding a distinct
XX member of the anti-Rhd polyclonal antibody, and one or more recombinase
XX recognition sequences. Methods are also provided for generating (M2) a
XX polyclonal working cell bank; manufacturing (M3) an anti-Rhd recombinant
XX polyclonal antibody. In (M1), the library of anti-Rhd antibody expression
XX vectors encodes an anti-Rhd recombinant polyclonal antibody where at
XX least one of the individual members specifically bind to eph3, eph4, and
XX eph9 (Rhd category VI antigen) and further members alone or in
XX combination bind to the remaining Rhesus D antigen epitopes eph1, eph2,
XX eph5, eph6/7 and eph8. The single copy of a nucleic acid segment encoding
XX a distinct member of the anti-Rhd polyclonal, is integrated in a single
XX predefined genomic locus of each individual cell in the collection of
XX cells, the locus being capable of mediating high-level expression of each
XX member of the recombinant polyclonal antibody. (M1) is useful for
XX generating a collection of cells suitable as manufacturing cell line for
XX expression of an anti-Rhesus D (Rhd) recombinant polyclonal antibody. An
XX anti-Rhd recombinant polyclonal antibody (A1) obtained by the method is
XX useful for the treatment, amelioration or prophylaxis in an animal. (A1)
XX is also useful for the preparation of a composition for the prophylaxis
XX of hemolytic disease of the newborn, treatment of idiopathic
XX thrombocytopenic purpura (ITP), or prevention of sensitization to the
XX Rhesus D antigen after transfusions of Rhd(+) blood to Rhd(-)
XX individuals. (A1) is useful for the diagnosis of the hemolytic diseases.
XX (M1) generates recombinant polyclonal antibody from a single cell line,
XX as a single batch, and provides a superior replacement of plasma-derived
XX prophylactic and therapeutic immunoglobulin products. The present
XX sequence represents the amino acid sequence of the light chain (LC)
XX region of an anti-Rhd Fab clone (see descriptive line for the clone
XX name).
XX
SQ Sequence 214 AA;
XX
Query Match 87.5%; Score 475; DB 10; Length 214;
Best Local Similarity 87.7%; Pred. No. 2.5e-28;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNYYQHKRGKAPKLLIYAASSLGVSRSR 60

```

DB 3 QLTQSPSSLSASVGDHVTITCRASQSSISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 62
 QY 61 SSGSGYTDFTLTITSSLOPEDFATYYCOESISASYTFGCGTKVEIKR 106
 DB 63 SSGSGTDFTLTITSSLOPEDFATYYCOQSYSTPWTFGCGTKVEIKR 108

RESULT 7

AAG93667
 ID AAG93667 standard; protein; 107 AA.

AC AAG93667;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH54 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens;

PN US625455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2001-388931/41.

DR N-PSDB; AAH68724.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.

PS Claim 1; Col 70; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.

CC (I) are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

XX SQ Sequence 107 AA;

Query Match

Best Local Similarity 87.3%; Score 474; DB 4; Length 107;
 Pred. No. 1.6e-28;

Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDHVTITCRASQSSISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

DB 2 ELTQSPSSLSASVGDHVTITCRASQSSISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYTDFTLTITSSLOPEDFATYYCOESISASYTFGCGTKVEIKR 106

DB 62 SSGSGTDFTLTITSSLOPEDFATYYCOQSYSTPWTFGCGTKVEIKR 107

RESULT 8

ABO27474
 ID ABO27474 standard; protein; 107 AA.

AC ABO27474;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH54.

KW Human; RH(D) binding protein; blood typing; blood product; antibody;
 magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2003-512273/48.

DR N-PSDB; ACD45388.

PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.

PS Claim 4; Page 53; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents the amino acid sequence of a human anti-Rh(D) chain

XX SQ Sequence 107 AA;

Query Match

Best Local Similarity 87.3%; Score 474; DB 6; Length 107;
 Pred. No. 1.6e-28;

Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDHVTITCRASQSSISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60

DB 2 ELTQSPSSLSASVGDHVTITCRASQSSISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYTDFTLTITSSLOPEDFATYYCOESISASYTFGCGTKVEIKR 106

DB 62 SSGSGTDFTLTITSSLOPEDFATYYCOQSYSTPWTFGCGTKVEIKR 107

RESULT 9

AEB74551

ID AEB74551 standard; protein; 107 AA.

AC AEB74551;

DT 23-FEB-2006 (first entry)

DE Anti-Rh(D) light chain SH54, SEQ ID 179.

KW Rh(D); erythrocyte; tissue typing; transplantation; light chain.

OS Synthetic.

PN US2005282252-A1.

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XX 22-DEC-2005.
PD
XX 22-FEB-2005; 2005US-00064174.
PF
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX (SIEG/) SIEGEL D L.
XX
XX Siegel DL;
XX
XX WPI; 2006-046435/05.
DR N-PSDB; ABE74594.
XX
XX New RH(D)-binding proteins, useful for typing donor white blood cells for
PT human leukocyte antigens for the purposes of matching donors and
PT recipients for potential transplant matching in the case of both solid
PT organ or tissue transplanting.
XX
XX Claim 5; SEQ ID NO 179; 999P; English.
XX
XX The present invention relates to novel Rh(D) antibody light and heavy
CC chains. The antibody heavy chains are given in ABE74373-ABE74400 and
CC ABE74511-ABE74525. The antibody light chains are given in ABE74398-
CC ABE74441 and ABE74526-ABE74553. The Rh(D) antigen is a red blood cell
CC membrane protein. The antibodies are useful for typing donor white blood
CC cells for human leukocyte antigen (HLA) antigens for the purposes of
CC matching donors and recipients for potential transplant matching in the
CC case of both solid (for example, kidney, heart, liver, lung) and non-
CC solid (for example, bone marrow) organ or tissue transplanting. The
CC present sequence is one such antibody light chain.
XX
XX Sequence 107 AA;
SQ
Query Match 87.3%; Score 474; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-28;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPKLLIYAASSLQSGVPSRF 60
DB 2 ELTQSPSSMSASVGBRVITTCRASQSIGTYLNWYQOKPKAKPKLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYGTDFLTLLTISLQPEDFATYCCQOSYSTPMTFGQGTVEIKR 106
DB 62 SSGSGGTDFLTLLTISLQPEDFATYCCQOSYSTPMTFGQGTVEIKR 107

RESULT 10
AAG93663
ID AAG93663 standard; protein; 107 AA.
XX
XX AAG93663;
AC
XX 14-SEP-2001 (first entry)
DT
XX Human anti-Rh(D) antibody clone SH49 protein sequence.
DE
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX OS
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 27-JUN-1997; 97US-00884045.

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PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
DR N-PSDB; AAH68720.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 69; 162P; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (1) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
SQ
Sequence 107 AA;
Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAKPKLLIYAASSLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITTCRASQSIGTYLNWYQOKPKAKPKLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYGTDFLTLLTISLQPEDFATYCCQOSYSTPMTFGQGTVEIKR 106
DB 62 SSGSGGTDFLTLLTISLQPEDFATYCCQOSYSTPMTFGQGTVEIKR 107

RESULT 11
AAG93664
ID AAG93664 standard; protein; 107 AA.
XX
XX AAG93664;
AC
XX 14-SEP-2001 (first entry)
DT
XX Human anti-Rh(D) antibody clone SH50 protein sequence.
DE
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX OS
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68721.

```

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.

XX Claim 1; Col 69; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein.
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRVTISCRASORINTYLMNVOHKPGKAPKLLIYAASLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVRVTITCRASQSISSYLMNVOQKPGKAPKLLIYAASLSQGVPSRF 61
QY 61 SGGSGYGTDFTLTITSSIQFEDFASVYCOESLSASVYTGQGTKEIKR 106
DB 62 SGGSGYGTDFTLTITSSIQFEDFATVYCOQSYSTLWTFGQGTKEIKR 107

RESULT 12
AAG93590
ID AAG93590 standard; protein; 107 AA.

XX AAG93590;

XX 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain I02 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Kn phenotype; diagnosis; therapeutic.

XX Homo sapiens.

XX US625455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI, 2001-388931/41.

XX N-PSDB; AAH68647.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.

XX Claim 1; Col 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein.

CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.3e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVRVTISCRASORINTYLMNVOHKPGKAPKLLIYAASLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVRVTITCRASQSISSYLMNVOQKPGKAPKLLIYAASLSQGVPSRF 61
QY 61 SGGSGYGTDFTLTITSSIQFEDFASVYCOESLSASVYTGQGTKEIKR 106
DB 62 SGGSGYGTDFTLTITSSIQFEDFATVYCOQSYSTLWTFGQGTKEIKR 107

RESULT 13
ABO27471
ID ABO27471 standard; protein; 107 AA.

XX ABO27471;

XX 12-SEP-2003 (first entry)

XX Anti-Rh(D) light chain SH50.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;
XX magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI, 2003-512273/48.

XX N-PSDB; ACD45385.

XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 52; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;

Best Local Similarity 86.8%; Pred. No. 2.3e-28; Indels 0; Gaps 0;
Matches 92; Conservative 7; Mismatches 7;

QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNWYQHKPKKLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVTCRASQSISSYLNWYQHKPKKLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGDFTLTISLSQFEDPASYYCOESLSASYTFGQGTKEIKR 106
DB 62 SSGSGYGDFTLTISLSQFEDPATYCCOQSYSTPWTFGQGTKEIKR 107

RESULT 14

ABO27397 standard; protein; 107 AA.

ABO27397;

12-SEP-2003 (first entry)

Anti-Rh(D) chain 102.

Human, RH(D) binding protein; blood typing; blood product; antibody;
magnetically activated cell sorting.

Homo sapiens.

US2003040605-A1.

27-FEB-2003.

04-MAY-2001; 2001US-00848798.

11-OCT-1996; 96US-0028550P.
27-JUN-1997; 97US-00884045.

10-APR-1998; 98US-0081380P.
29-JAN-1999; 99US-00240274.

(UYPE-) UNIV PENNSYLVANIA.

Siegel DL;

WPI; 2003-512273/48.

N-PSDB; ACD45311.

New human Rh(D)-binding protein useful for various diagnostic and
therapeutic applications, including typing of blood or blood products.

Claim 4; Page 26; 187pp; English.

The invention relates to an isolated Rh(D) binding protein. The protein
can be used for magnetically activated cell sorting. The protein is
useful in various diagnostic and therapeutic applications in humans,
including typing of blood or blood products. The present sequence
represents the amino acid sequence of a human anti-Rh(D) chain

Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;

Best Local Similarity 87.7%; Pred. No. 2.3e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNWYQHKPKKLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVTCRASQSISSYLNWYQHKPKKLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGDFTLTISLSQFEDPASYYCOESLSASYTFGQGTKEIKR 106
DB 62 SSGSGYGDFTLTISLSQFEDPATYCCOQSYSTPWTFGQGTKEIKR 107

QY 61 SSGSGYGDFTLTISLSQFEDPASYYCOESLSASYTFGQGTKEIKR 106
DB 62 SSGSGYGDFTLTISLSQFEDPATYCCOQSYSTPWTFGQGTKEIKR 107

QY 61 SSGSGYGDFTLTISLSQFEDPASYYCOESLSASYTFGQGTKEIKR 106
DB 62 SSGSGYGDFTLTISLSQFEDPATYCCOQSYSTPWTFGQGTKEIKR 107

RESULT 15

ABO27470

ID ABO27470 standard; protein; 107 AA.

ABO27470;

12-SEP-2003 (first entry)

Anti-Rh(D) light chain SH49.

Human, RH(D) binding protein; blood typing; blood product; antibody;
magnetically activated cell sorting.

Homo sapiens.

US2003040605-A1.

27-FEB-2003.

04-MAY-2001; 2001US-00848798.

11-OCT-1996; 96US-0028550P.
27-JUN-1997; 97US-00884045.

10-APR-1998; 98US-0081380P.
29-JAN-1999; 99US-00240274.

(UYPE-) UNIV PENNSYLVANIA.

Siegel DL;

WPI; 2003-512273/48.

N-PSDB; ACD45384.

New human Rh(D)-binding protein useful for various diagnostic and
therapeutic applications, including typing of blood or blood products.

Claim 4; Page 52; 187pp; English.

The invention relates to an isolated Rh(D) binding protein. The protein
can be used for magnetically activated cell sorting. The protein is
useful in various diagnostic and therapeutic applications in humans,
including typing of blood or blood products. The present sequence
represents the amino acid sequence of a human anti-Rh(D) chain

Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;

Best Local Similarity 86.8%; Pred. No. 2.3e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNWYQHKPKKLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVTCRASQSISSYLNWYQHKPKKLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGDFTLTISLSQFEDPASYYCOESLSASYTFGQGTKEIKR 106
DB 62 SSGSGYGDFTLTISLSQFEDPATYCCOQSYSTPWTFGQGTKEIKR 107

Search completed: August 30, 2006, 00:41:52

Job time : 96.2394 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 9.95758 Seconds
(without alignments)
1024.243 Million cell updates/sec

Title: US-10-027-725a-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDVTVTS.....QESLSASVTFGGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 80:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	85.5	127	2	S40367 Ig kappa chain V-J
2	459	84.5	123	2	S40331 Ig kappa chain - h
3	458	84.3	108	2	B49047 Ig kappa chain V r
4	456	84.0	108	2	S47182 Ig kappa chain - h
5	452	83.2	109	2	S31998 Ig kappa chain - h
6	452	83.2	109	2	S31979 Ig kappa chain - h
7	448	82.5	109	2	S31980 Ig kappa chain - h
8	446	82.1	108	2	S44122 Ig kappa chain V r
9	445	82.0	109	2	S32001 Ig kappa chain - h
10	441	81.2	108	2	S19674 Ig kappa chain V r
11	439	80.8	109	2	S31981 Ig kappa chain - h
12	439	80.8	129	2	S52793 Ig kappa chain V r
13	438	80.7	107	2	S36264 Ig lambda chain V
14	437	80.5	108	2	S31977 Ig kappa chain - h
15	436	80.3	109	2	S31983 Ig kappa chain - h
16	436	80.3	122	2	S40370 Ig kappa chain - h
17	436	80.3	129	1	K1HUKK Ig kappa chain pre
18	435	80.3	129	1	S40317 Ig kappa chain - h
19	435	80.1	128	2	S46372 Ig light chain var
20	434	79.9	120	2	S46370 Ig kappa chain V-J
21	433.5	79.8	105	2	S40315 Ig kappa chain - h
22	433	79.7	108	1	K1HUKK Ig kappa chain V-I
23	432	79.6	132	2	S40334 Ig kappa chain - h
24	431	79.4	109	2	S31978 Ig kappa chain - h
25	430	79.2	108	1	K1HUKK Ig kappa chain V-I
26	430	79.2	132	2	S38646 Ig kappa chain V r
27	425	78.3	122	2	S40314 Ig kappa chain - h
28	425	78.3	129	2	S40369 Ig kappa chain - h
29	424.5	78.2	106	2	PC2397 anti-tetanus toxin

30	423.5	78.0	124	2	S40336 Ig kappa chain V-J
31	422.5	77.8	107	2	S36275 Ig lambda chain V
32	422	77.7	125	2	S40333 Ig kappa chain V-J
33	422	77.7	131	2	S40352 Ig kappa chain V-J
34	420	77.3	108	1	K1HUKK Ig kappa chain V-I
35	420	77.3	125	2	S40349 Ig kappa chain V-J
36	420	77.3	126	2	S40335 Ig kappa chain V-J
37	419	77.2	125	2	S40350 Ig kappa chain - h
38	418	77.0	117	2	S46371 Ig kappa chain V r
39	418	77.0	129	2	S52792 Ig kappa chain V r
40	417	76.8	117	2	S46376 Ig kappa chain V-J
41	416	76.6	108	1	K1HUKK Ig kappa chain V-I
42	416	76.2	107	2	JL0139 Ig kappa chain V r
43	414	76.2	107	2	S36262 Ig lambda chain V
44	414	76.2	108	1	K1HUKK Ig kappa chain V-I
45	413.5	76.2	108	2	S30521 Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
A/Reference number: S40312; MIDID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
A/Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 464; DB 2; Length 127;
Best Local Similarity 84.9%; Pred. No. 2,6e-34;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY	1	ELTQSPSSLSASVGDVTVTSICRASORINTYINYOHKPKAPLILYAASSLQGVPSRF	60
DB	20	QMTQSPSSLSASVGVDRVITTCRASQSIINLYIMYOKKPKAPLILYAASSLQGVPSRF	79
QY	61	SGSGVGTDFLTITSSLOFEDFASVYCOESLSASVTFGGQTKVEIKR	106
DB	80	SGSGSGTDFLTITSSLOPEDFATVYCOGSYNTFWTGGQTKVEIKR	125

RESULT 2

S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
A/Reference number: S40312; MIDID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KLE>
A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 459; DB 2; Length 123;

Best Local Similarity 85.7%; Pred. No. 7e-34;
Matches 90; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKRGKAPKLLIYAASLSGVSRSR 60
Db 19 QMTQSPSSLSASVGDRTITICRASQSISSYLNWYQQRGKAPKLLIYAASLSGVSRSR 78
QY 61 GSGGYGTDFTLTITISLQPEDPASYCOESLSASYTFGQGTVEIKR 105
Db 79 GSGSGTDFLTITISLQPEDPASYCOOSYSTPTTFGQGTVEIKR 123

RESULT 3

Ig kappa chain V region (monoclonal seriatonal autoantibody StrAB SA-1A) - human (fragm
B49047
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal seriatonal autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44
A/Experimental source: thymic B lymphocytes
A/Note: Sequence extracted from NCBI backbone (NCBI:113208, NCBI:113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 458; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 7.6e-33;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKRGKAPKLLIYAASLSGVSRSR 60
Db 3 QMTQSPSSLSASVGDRTITICRASQSISSYLNWYQQRGKAPKLLIYAASLSGVSRSR 62
QY 61 GSGGYGTDFTLTITISLQPEDPASYCOESLSASTFGQGTVEIKR 106
Db 63 GSGSGTDFLTITISLQPEDPASYCOOSYSTPTTFGQGTVEIKR 108

RESULT 4

Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S47182
R/McInosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
Submitted to the EMBL Data Library, June 1994
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A/Reference number: S47181
A/Accession: S47182
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <MCI>
A/Cross-references: UNIPARC:UPI00001161E5; EMBL:X79786; NID:G506422; PTDN:CAA56182.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKRGKAPKLLIYAASLSGVSRSR 60
Db 3 ELTQSPSSLSASVGDRTITICRASQSISSYLNWYQQRGKAPKLLIYAASLSGVSRSR 62
QY 61 GSGGYGTDFTLTITISLQPEDPASYCOESLSASYTFGQGTVEIKR 106

Db 63 GSGSGTDFLTITISLQPEDPASYCOOSYSTPTTFGQGTVEIKR 108

RESULT 5

Ig kappa chain - human (fragment)
S3198
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S3198
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31977
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <FOR>
A/Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:G38501; PTDN:CAA78790.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;
Best Local Similarity 83.8%; Pred. No. 2.6e-33;
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKRGKAPKLLIYAASLSGVSRSR 61
Db 4 MTQSPSSLSASVGDRTITICRASQSISSYLNWYQQRGKAPKLLIYAASLSGVSRSR 63
QY 62 GSGGYGTDFTLTITISLQPEDPASYCOESLSASYTFGQGTVEIKR 106
Db 64 GSGSGTDFLTITISLQPEDPASYCOOSYSTPTTFGQGTVEIKR 108

RESULT 6

Ig kappa chain - human (fragment)
S31979
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31979
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31979
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <FOR>
A/Cross-references: UNIPARC:UPI0000116492; EMBL:Z15075; NID:G38489; PTDN:CAA78784.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;
Best Local Similarity 81.9%; Pred. No. 2.6e-33;
Matches 86; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKRGKAPKLLIYAASLSGVSRSR 61
Db 4 MTQSPSSLSASVGDRTITICRASQSISSYLNWYQQRGKAPKLLIYGTSLTSLGVSRSR 63
QY 62 GSGGYGTDFTLTITISLQPEDPASYCOESLSASYTFGQGTVEIKR 106
Db 64 GSGSGTDFLTITISLQPEDPASYCOOSYSTPTTFGQGTVEIKR 108

RESULT 7

Ig kappa chain - human (fragment)
S31980
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S31980; S32000
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 C/Species: Homo sapiens (man)
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C/Accession: S32001
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 448; DB 2; Length 109;
 Best Local Similarity 81.0%; Pred. No. 5.9e-33;
 Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 61
 :|||||
 DB 4 MTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYGTSTLSGVSRRS 63
 C/Accession: S44122
 R/Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 submitted to the EMBL Data Library, March 1994
 C/Keywords: idiotype vaccination against human B-cell lymphoma: rescue of variable r
 A/Reference number: S44105
 A/Accession: S44122
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-108 <HAM>
 A/Cross-references: UNIPARC:UPI0000116630; EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PI
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

RESULT 8
 S44122

Ig kappa chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S44122
 R/Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 submitted to the EMBL Data Library, March 1994
 C/Keywords: idiotype vaccination against human B-cell lymphoma: rescue of variable r
 A/Reference number: S44105
 A/Accession: S44122
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-108 <HAM>
 A/Cross-references: UNIPARC:UPI0000116630; EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PI
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 446; DB 2; Length 108;
 Best Local Similarity 83.0%; Pred. No. 8.7e-33;
 Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 60
 :|||||
 DB 3 QMTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYASLSGVSRRS 62
 C/Accession: S31981
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

RESULT 9
 S32001

Ig kappa chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C/Accession: S32001
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

A/Accession: S32001
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-109 <POR>

A/Cross-references: UNIPARC:UPI0000116498; EMBL:Z15082; NID:938503; PIDN:CAA78791.1; PID
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 445; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 1.1e-32;
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 61
 :|||||
 DB 4 MTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYGTSTLSGVSRRS 63
 C/Accession: S19674
 R/Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
 J. Mol. Biol. 222, 581-597, 1991
 A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
 A/Reference number: S19663; NID:92085276; PMID:1748994
 A/Accession: S19674
 A/Molecule type: mRNA
 A/Residues: 1-108 <MAR>
 A/Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:937860; PIDN:CAA43823.1; PID
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 441; DB 2; Length 108;
 Best Local Similarity 82.9%; Pred. No. 2.4e-32;
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 61
 :|||||
 DB 4 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 63
 C/Accession: S31981
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 3.7e-32;
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 61
 :|||||
 DB 4 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 63
 C/Accession: S31981
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 3.7e-32;
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 61
 :|||||
 DB 4 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 63
 C/Accession: S31981
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 3.7e-32;
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 61
 :|||||
 DB 4 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASSLSGVSRRS 63
 C/Accession: S31981
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 submitted to the EMBL Data Library, June 1992
 C/Keywords: lack of promiscuity in autoantigen-specific H and L chain combinations as
 F;16-90/Domain: immunoglobulin homology <IMM>

KM Immunoglobulin domain.
 FT NON_TER 1
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
 Query Match 85.6%; Score 465; DB 2; Length 108;
 Best Local Similarity 84.9%; Pred. No. 7.2e-42;
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTISCRASQRIINTYLMYQHKGPKAPKLLIYAASSLSQSVSRF 60
 DB 3 QMTQSPSSLSASVGDRTTITCRASQSISSYLMYQOKPGKAPKLLIYAASSLSQSVSRF 62
 QY 61 SSGSGYGFDTLTISLQFEDFASYSYCOESLSASYSYFGCGTKVEIKR 106
 DB 63 SSGSGYGFDTLTISLQFEDFASYSYCOESLSASYSYFGCGTKVEIKR 108

RESULT 2
 ID Q96SA9_HUMAN PRELIMINARY; PRT; 107 AA.
 AC Q96SA9; 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=98375893; PubMed=9712075.
 RA Adderson E.B., Shikman A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
 RT antibody V region genes";
 RT Eur. J. Immunol. 16:12020-2031(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92387224; PubMed=1516616;
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
 RT "Human monoclonal strictional autoantibodies isolated from thymic B
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene
 RT segments associated with the autoimmune repertoire";
 RT Eur. J. Immunol. 22:2231-2236(1992).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93170387; PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation";
 RT Eur. J. Immunol. 23:391-397(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
 RA Manheimer-Loty A., Katz J.B., Pillingner M., Gnossein C., Smith A.,
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idiotype";
 RT Eur. J. Exp. Med. 174:1639-1652(1991).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91243737; PubMed=1903706;
 RA Blaison G., Kuntz J.L., Pasquali J.L.;
 RT "Molecular analysis of V kappa III variable regions of polyclonal
 RT rheumatoid factors during rheumatoid arthritis";
 RT Eur. J. Immunol. 21:1221-1227(1991).
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 CC EMBL: U96396; AAB6785.1; -, mRNA.
 DR PIR: B49047; B49047.
 DR PIR: PH0867; PH0867.
 DR PIR: S16840; S16840.
 DR PIR: S31977; S31977.
 DR PIR: S34083; S34083.
 DR PIR: S34086; S34086.
 DR HSSP: P01607; 1BMW.
 DR SMR: Q96SA9; 1-107.
 DR Ensemble: ENSG00000163245; Homo sapiens.
 DR LinkHub; Q96SA9; -.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1-like.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KM Immunoglobulin domain.
 FT NON_TER 1
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;
 Query Match 82.8%; Score 449.5; DB 2; Length 107;
 Best Local Similarity 84.9%; Pred. No. 3.3e-40;
 Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTTISCRASQRIINTYLMYQHKGPKAPKLLIYAASSLSQSVSRF 60
 DB 3 QMTQSPSSLSASVGDRTTITCRASQSISSYLMYQOKPGKAPKLLIYAASSLSQSVSRF 62
 QY 61 SSGSGYGFDTLTISLQFEDFASYSYCOESLSASYSYFGCGTKVEIKR 106
 DB 63 SSGSGYGFDTLTISLQFEDFASYSYCOESLSASYSYFGCGTKVEIKR 107

RESULT 3
 ID Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
 AC Q9UL81; 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=98277135; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Barney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
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 CC EMBL: AF035033; AAD56269.1; -, mRNA.
 DR HSSP: P01607; 1BMW.
 DR SMR: Q9UL81; 1-107.
 DR LinkHub; Q9UL81; -.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG_1-like.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
Query Match 80.9%; Score 439.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 3.9e-39;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;
QY 1 ELTQSPSSLSASVGDVITTCRASQRIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDVITTCRASQSIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 62
QY 61 SGSGYGTDFTLTITSSLOFEDFASYYCOESLSASVTFGQTKVEIKR 106
DB 63 SGSGGTDFTLTITSSLOFEDFATYYCOQSYSA-LTRPGPKVDIKR 107
RESULT 4
O6GMXO HUMAN PRELIMINARY; PRT; 236 AA.
AC O6GMXO;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.L.
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC EMBL; BC073775; AAH73775.1; -; mRNA.
DR SMR; Q6GMXO; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

DR InterPro; IPR033106; V-set.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E928BF8 CRC64;
Query Match 80.8%; Score 439; DB 2; Length 236;
Best Local Similarity 81.1%; Pred. No. 1.1e-38;
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVITTCRASQRIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60
DB 25 QMTQSPSSLSASVGDVITTCRASQSIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 84
QY 61 SGSGYGTDFTLTITSSLOFEDFASYYCOESLSASVTFGQTKVEIKR 106
DB 85 SGSGGTDFTLTITSSLOFEDFATYYCOQSYNIPTRPGGTVEIKR 130
RESULT 5
KV1W HUMAN STANDARD; PRT; 129 AA.
ID KV1W HUMAN
AC P04431;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrist G., Zachau H.G.,
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC EMBL; X00965; CAA25477.1; ALU_TERM; Genomic DNA.
CC PIR; A01883; K1HWK.
DR HSSP; P04431; 23-129.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR033106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 23
FT REGION 23 45 Ig kappa chain V-I region Walker.
FT REGION 46 56 Framework-1.
FT REGION 57 71 Complementarity-determining-1.
FT REGION 72 78 Framework-2.
FT REGION 79 110 Complementarity-determining-2.
FT REGION 111 119 Complementarity-determining-3.

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FT REGION 120 129 Framework-4.
FT DISUPID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC29 CRC64;
Query Match 80.3%; Score 436; DB 1; Length 129;
Best Local Similarity 81.9%; Pred. No. 1.2e-38;
Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTITICRASQSIINTYLNWYQHKGPKAPKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGYGTDFLTITSSLOFEDFASYSYQESLSASYTFGQGTKEIKR 105
DB 85 SSGSGYGTDFLTITSSLOFEDFASYSYQESLSASYTFGQGTKEIKR 129

RESULT 6
O6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.
AC O6GMX8;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 17.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshinsky S., Carninci P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: BC073764; AAH73764.1; -; mRNA.
DR SRR: O6GMX8; 24-235.
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.

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DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; Cl-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGcl; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN; 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
Query Match 80.3%; Score 436; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 2.3e-38;
Matches 85; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITICRASQRIINTYLNWYQHKGPKAPKLLIYAASSLSQGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTITICRASQSIINTYLNWYQHKGPKAPKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGYGTDFLTITSSLOFEDFASYSYQESLSASYTFGQGTKEIKR 106
DB 85 SSGSGYGTDFLTITSSLOFEDFASYSYQESLSASYTFGQGTKEIKR 130

RESULT 7
O6GMW1 HUMAN PRELIMINARY; PRT; 236 AA.
AC O6GMW1;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 17.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshinsky S., Carninci P., Prange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: BC073791; AAH73791.1; -; mRNA.
DR SRR: O6GMW1; 24-236.
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SQUONCE 236 AA; 25751 MW; 5BFEGA087APAC437 CRC64;

Query Match 79.9%; Score 434; DB 2; Length 236;
Best Local Similarity 81.1%; Pred. No. 3, 8e-38;
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPGKAPKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGYGFDTLTITSSLPEDFASVYCOESLSASTFEGGKVEIKR 106
DB 85 SSGSGYGFDTLTITSSLPEDFATYTCDDYNYPTWTFGQKVEIKR 130

RESULT 8
KVLE_HUMAN STANDARD; PRT; 108 AA.
ID PO1597;
AC 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DE 07-MAR-2006, entry version 39.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=7205133; PubMed=5124396;
RA Milstein C.P., Deverton E.V.,
RT "The amino acid sequence of a human kappa light chain."
RL Biochem J 123:945-958(1971).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
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PIR; A01865; K1HNDU.
DR HSSP; PO1607; 1BMW.
DR SMR; PO1597; 4-108.
DR GO; GO:0005576; C:extracellular region; NMS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
KW CHAIN 1
FT 1 >108
FT REGION 1 23 Ig kappa chain V-I region DEE.
FT REGION 24 34 Framework-1.
FT REGION 35 49 Complementarity-determining-1.
FT REGION 50 56 Framework-2.
FT REGION 57 88 Complementarity-determining-2.
FT REGION 88 Framework-3.

FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDDGE350017F1BS1 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;
Best Local Similarity 77.4%; Pred. No. 2e-38;
Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 3 ZMTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPGKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGYGFDTLTITSSLPEDFASVYCOESLSASTFEGGKVEIKR 106
DB 63 SSGSGYGFDTLTITSSLPEDFATYTCDDYNYPTWTFGQKVEIKR 130

RESULT 9
KVLE_HUMAN STANDARD; PRT; 108 AA.
ID PO1600;
AC 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DE 07-MAR-2006, entry version 44.
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.,
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones protein Hau): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
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PIR; A01868; K1HNDU.
DR PDB; 1F6L; X-ray; L=1-89.
DR GO; GO:0005576; C:extracellular region; NMS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
KW CHAIN 1
FT 1 >108
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
FT STRAND 4 7

FT STRAND 9 12
 FT TURN 15 16
 FT STRAND 19 27
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT STRAND 77 77
 FT STRAND 80 82
 FT STRAND 84 90
 FT STRAND 92 95
 FT STRAND 98 98
 FT STRAND 102 105
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.2%; Score 430; DB 1; Length 108;
 Best Local Similarity 78.3%; Pred. No. 4.2e-38;
 Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLMWQHKGPKAPKLLIYAASSLQSGVPSRF 60
 Db 3 QMTQSPSSLSASVGDVITITCRASQISISYLSWYQKPKAPQVLIYAASSLPQSGVPSRF 62
 QY 61 SSGSGYGTDFLTITSSIQFEDFPASYCOESLSASYTFGCGTKVEIKR 106
 Db 63 SSGSGGTDFLTITSSIQFEDFPATYCCQNLNSPPTGGGTKVEIKR 108

RESULT 10
 Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q6PIH7;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 17.
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Araminci F., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Vallation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RP NIH MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC034141; AAH34141.1; -; mRNA.
 DR HSSP; P01607; IAR2.
 DR SMR; Q6PIH7; 23-236.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 78.1%; Score 424; DB 2; Length 236;
 Best Local Similarity 80.2%; Pred. No. 4.5e-37;
 Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLMWQHKGPKAPKLLIYAASSLQSGVPSRF 60
 Db 25 QLTQSPSSLSASVGDVITITCRASQGISYLAWYQKPKAPKLLIYAASSLPQSGVPSRF 84
 QY 61 SSGSGYGTDFLTITSSIQFEDFPASYCOESLSASYTFGCGTKVEIKR 106
 Db 85 SSGSGGTDFLTITSSIQFEDFPATYCCQNLNSPPTGGGTKVEIKR 130

RESULT 11
 Q9UL79_HUMAN PRELIMINARY; PRT; 108 AA.
 AC Q9UL79;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC MEDLINE=98277119; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=92289816; PubMed=1601042;
 RA Huber C., Klobbeck H.G., Zachau H.G.;
 RT "Ongoing V kappa-J kappa recombination after formation of a productive
 RT V kappa-J kappa coding joint."
 RT Eur. J. Immunol. 22:1561-1565(1992).
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=93170387; PubMed=8436174;
 RA Wagner S.D., Lutzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are

RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation."
 RL Eur. J. Immunol. 23:391-397(1993).
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 CC -----
 CC EMBL: AF035035; AAD56271.1; -; mRNA.
 DR PIR: S23638; S23638.
 DR PIR: S30521; S30521.
 DR PIR: S34090; S34090.
 DR HSSP: P01607; 1BMW.
 DR LinkHub; Q9UL79; 1-108.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR InterPro: IPR013106; V-set.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin domain.
 FT NON TER 1
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;
 Query Match 77.7%; Score 422; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 3e-37; Mismatches 14; Indels 0; Gaps 0;
 Matches 84; Conservative 7;
 QY 2 LTQSPSSLSASVGDVVTISCRASQRIINTYLNMYQHKPKAPKLLIYAASLSQGVPSRF 61
 Db 4 MTQSPSLASSTQDVRVITSCRMGSGISSTYLAWYQKRGKAPPELLIYAASLTQGVPSRF 63
 QY 62 GSGYGDTFTLTITSLQFDPASVYCOESLSASTFGQGTVEIKR 106
 Db 64 GSGSGTDFLTITSLQSEDFATYCCQYSPFPFGQGTVEIKR 108
 RESULT 12
 ID KVIN_HUMAN STANDARD; PRT; 108 AA.
 AC P01606;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 07-MAR-2006, entry version 39.
 DE Ig kappa chain V-I region OU.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains".
 RL Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
 CC macroglobulin.
 CC -----
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 CC -----
 CC PIR: A01872; K1HUOU.
 DR HSSP: P01607; 1BMW.
 DR LinkHub; P01606; -;
 DR GO: GO:0005576; C:extracellular region; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR003599; Ig.

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig V.
 DR InterPro: IPR013106; V-set.
 DR Pfam: PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin domain;
 KM Immunoglobulin V region.
 FT CHAIN 1
 FT REGION 1 23
 FT REGION 24 34
 FT REGION 35 49
 FT REGION 50 56
 FT REGION 57 88
 FT REGION 89 97
 FT REGION 98 107
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11779 MW; 8283D4A24105827E CRC64;
 Query Match 77.3%; Score 420; DB 1; Length 108;
 Best Local Similarity 68.9%; Pred. No. 5e-37; Mismatches 11; Indels 0; Gaps 0;
 Matches 73; Conservative 22;
 QY 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNMYQHKPKAPKLLIYAASLSQGVPSRF 60
 Db 3 QMTZSSSSLSASVGBVVTITCRASZTISLYBMVZKPKGAPPELLIYAASBLHSGVPSRF 62
 QY 61 SSGSGTDFLTITSLQFDPASVYCOESLSASTFGQGTVEIKR 106
 Db 63 SSGSGTDFLTITSLQSEDFATYCCQYSPFPFGQGTVEIKR 108
 RESULT 13
 ID Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
 AC Q9UL70;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 22.
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,
 RA Diamond B.;
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 associated idiotype".
 RL J. Exp. Med. 174:1639-1652(1991).
 CC -----
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 CC -----
 CC EMBL: AF035044; AAD56280.1; -; mRNA.
 DR PIR: PH0863; PH0863.
 DR HSSP: P01607; 1BMW.
 DR SMR: Q9UL70; 1-108.
 DR InterPro: IPR003599; Ig.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
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Query Match 77.3%; Score 420; DB 2; Length 108;
Best Local Similarity 79.2%; Pred. No. 5e-37;
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTYTICRASQRIINTYLNWYQHKGAPKLLIYAASLQSGVPSRF 60
DB 3 QMTQSPSLASVGDRTYTICRASQGISNLYAWYQKPKGKPKSLIYAASLTQSGVPSRF 62
QY 61 GSGSGYTDFTLTISLQPEDPASYCOESLSASYTFQGTKEIKR 106
DB 63 GSGSGYTDFTLTISLQPEDVATYCCQKNSAPRTFPGTKLEIKR 108

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ID Q72473_HUMAN
AC Q72473;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE IGKC protein.
GN Name=IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Muliyil S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
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CC EMBL; BC056256; AAH56256.1; -, mRNA.
DR HSSP; P01834; 1HEZ.

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DR SMR: Q72473; 22-234.
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00407; IgC1; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
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DB 24 MTQSPSLASVGDRTYTICRASQGISNLYAWYQKPKGKPKSLIYAASLTQSGVPSRF 63
QY 62 GSGSGYTDFTLTISLQPEDPASYCOESLSASYTFQGTKEIKR 106
DB 84 GSGSGYTDFTLTISLQPEDPASYCCQKYTYPTFPGTKLEIKR 128

RESULT 15
KVLF_HUMAN STANDARD; PRT; 108 AA.
ID KVLF_HUMAN
AC P01598;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RX MEDLINE=71064023; PubMed=5489770;
RA Gotlib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC PTR: A90562; KIHUEU.
DR HSSP; P01598; 1BMW.
DR SMR; P01598; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.

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DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
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 KW Immunoglobulin V region.
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 FT REGION 24 34 /Frid=PRO_0000059742.
 FT REGION 35 49 Framework-1.
 FT REGION 50 56 Complementarity-determining-1.
 FT REGION 57 88 Framework-2.
 FT REGION 89 97 Complementarity-determining-2.
 FT REGION 98 107 Framework-3.
 FT DISUPID 23 Complementarity-determining-3.
 FT NON_TER 23 88 Framework-4.
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.6%; Score 416; DB 1; Length 108;
 Best Local Similarity 77.1%; Pred. No 1.3e-36;
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 QY 61 SSGSGYGTDFLTITSSLOFEDPFASYCCQESLSASYTFGGGTRVEIK 105
 Db 63 IGSQSGTEFTLTITSSLOPDDPATYYCQQYNDSKMFQGGTRVEIK 107

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OM protein - protein search, using sw model

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(without alignments)
641.891 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543
Sequence: 1 ERTQSPSSIASVGVDRVTIS.....QESLSASYFGQGTKEIKR 106

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/prodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/H_COMB.pep:*
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6: /EMC_Celerra_SIDS3/prodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475	87.5	107	1	US-08-276-852-104 Sequence 104, App
2	475	87.5	107	1	US-08-899-575-104 Sequence 104, App
3	475	87.5	107	1	US-08-899-575-104 Sequence 104, App
4	475	87.5	107	5	PCT-US95-08743-104 Sequence 104, App
5	474	87.3	107	2	US-09-240-274-179 Sequence 179, App
6	474	87.3	107	2	US-09-848-798-179 Sequence 179, App
7	472	86.9	107	2	US-09-240-274-33 Sequence 33, App
8	472	86.9	107	2	US-09-240-274-175 Sequence 175, App
9	472	86.9	107	2	US-09-848-798-176 Sequence 176, App
10	472	86.9	107	2	US-09-848-798-175 Sequence 175, App
11	472	86.9	107	2	US-09-848-798-176 Sequence 176, App
12	472	86.9	107	2	US-09-848-798-176 Sequence 176, App
13	471	86.7	107	2	US-09-240-274-156 Sequence 156, App
14	471	86.7	107	2	US-09-848-798-156 Sequence 156, App
15	468	86.2	107	2	US-09-240-274-36 Sequence 36, App
16	468	86.2	107	2	US-09-848-798-36 Sequence 36, App
17	467	86.0	107	1	US-08-276-852-105 Sequence 105, App
18	467	86.0	107	1	US-08-899-575-105 Sequence 105, App
19	467	86.0	107	1	US-08-899-575-105 Sequence 105, App
20	467	86.0	107	5	PCT-US95-08743-105 Sequence 105, App
21	464.5	85.5	108	2	US-09-240-274-32 Sequence 32, App
22	464.5	85.5	108	2	US-09-240-274-43 Sequence 43, App
23	464.5	85.5	108	2	US-09-848-798-32 Sequence 32, App
24	464.5	85.5	108	2	US-09-848-798-43 Sequence 43, App
25	464	85.5	107	2	US-09-240-274-37 Sequence 37, App
26	464	85.5	107	2	US-09-848-798-37 Sequence 37, App

27	464	85.5	240	2	US-09-192-854-2 Sequence 2, App
28	464	85.5	240	2	US-09-511-939-2 Sequence 2, App
29	462	85.1	107	2	US-09-240-274-38 Sequence 38, App
30	462	85.1	107	2	US-09-240-274-39 Sequence 39, App
31	462	85.1	107	2	US-09-848-798-38 Sequence 38, App
32	462	85.1	107	2	US-09-848-798-39 Sequence 39, App
33	461	84.9	107	2	US-09-240-274-158 Sequence 158, App
34	461	84.9	107	2	US-09-848-798-158 Sequence 158, App
35	460.5	84.8	108	2	US-09-240-274-167 Sequence 167, App
36	460.5	84.8	108	2	US-09-848-798-167 Sequence 167, App
37	459.5	84.6	108	2	US-09-240-274-163 Sequence 163, App
38	459.5	84.6	108	2	US-09-848-798-163 Sequence 163, App
39	458	84.3	107	2	US-09-240-274-35 Sequence 35, App
40	458	84.3	107	2	US-09-240-274-173 Sequence 173, App
41	458	84.3	107	2	US-09-848-798-35 Sequence 35, App
42	458	84.3	107	2	US-09-848-798-173 Sequence 173, App
43	458	84.3	108	1	US-08-379-057-29 Sequence 29, App
44	457	84.2	104	1	US-08-276-852-106 Sequence 106, App
45	457	84.2	104	1	US-08-899-575-106 Sequence 106, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
Sequence 104, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbae, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGTDFLTITSSLOPEDFASYCOESLSASTTFCQGTKEIKR 106
Db 61 SSGSGTDFLTITSSLOPEDFATYCCOOSYSTPYTFQGTKEIKR 106

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 435
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGTDFLTITSSLOPEDFASYCOESLSASTTFCQGTKEIKR 106
Db 61 SSGSGTDFLTITSSLOPEDFATYCCOOSYSTPYTFQGTKEIKR 106

RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60

RESULT 4
PCT-US95-08743-104

Sequence 104, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-104

Query Match 87.5%; Score 475; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,4e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDVVTITCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
Qy 61 SGGSGTDFLTITSSLOQFDPFASYCOESLSASYTFGQTKVEIKR 106
Db 61 SGGSGTDFLTITSSLOQFDPFATYTCQSYSTPTFGQTKVEIKR 106

RESULT 5
US-09-240-274-179

Sequence 179, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match 87.3%; Score 474; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,8e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
Qy 61 SGGSGTDFLTITSSLOQFDPFASYCOESLSASYTFGQTKVEIKR 106
Db 61 SGGSGTDFLTITSSLOQFDPFATYTCQSYSTPTFGQTKVEIKR 106

Db 62 SGGSGTDFLTITSSLOQFDPFATYTCQSYSTPTFGQTKVEIKR 107

RESULT 6
US-09-848-798-179

Sequence 179, Application US/09848798
Patent No. 6858719
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match 87.3%; Score 474; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,8e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
Qy 61 SGGSGTDFLTITSSLOQFDPFASYCOESLSASYTFGQTKVEIKR 106
Db 62 SGGSGTDFLTITSSLOQFDPFATYTCQSYSTPTFGQTKVEIKR 107

RESULT 7
US-09-240-274-33

Sequence 33, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 2,8e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSIISYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOOSYSTLMTFGQGTVEIKR 107

RESULT 8

US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITSCRASORINTYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTOSPSLSASVGDRTVITSCRASQSSISYLMWYQOKKPKAPKLLIYAASSLSQGVPSRF 61
Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOOSYSTLMTFGQGTVEIKR 107

RESULT 9

US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITSCRASORINTYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTOSPSLSASVGDRTVITSCRASQSSISYLMWYQOKKPKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOOSYSTLMTFGQGTVEIKR 107

RESULT 10

US-09-848-798-33
; Sequence 33, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.8e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITSCRASORINTYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTOSPSLSASVGDRTVITSCRASQSSISYLMWYQOKKPKAPKLLIYAASSLSQGVPSRF 61
Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOOSYSTLMTFGQGTVEIKR 107

RESULT 11

US-09-848-798-175
; Sequence 175, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Best Local Similarity 86.8%; Pred. No. 2.8e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVYTFGQGTKEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYYCQGSYSTPTWTFGQGTKEIKR 107

RESULT 12
US-09-848-798-176
Sequence 176, Application US/09848798
Patent No. 6858719

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match
Best Local Similarity 86.9%; Score 472; DB 2; Length 107;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVYTFGQGTKEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYYCQGSYSTPTWTFGQGTKEIKR 107

RESULT 13
US-09-240-274-156
Sequence 156, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 156
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13

US-09-240-274-156

Query Match
Best Local Similarity 86.7%; Score 471; DB 2; Length 107;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVYTFGQGTKEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYYCQGSYSTPTWTFGQGTKEIKR 107

RESULT 14
US-09-848-798-156
Sequence 156, Application US/09848798
Patent No. 6858719

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 156
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match
Best Local Similarity 86.7%; Score 471; DB 2; Length 107;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVYTFGQGTKEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYYCQGSYSTPTWTFGQGTKEIKR 107

RESULT 15
US-09-240-274-36
Sequence 36, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 36
LENGTH: 107
TYPE: PRT

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 60,7091 Seconds
(without alignments)
808,788 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGRVITIS.....QESLSASYFGQGTKEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/Ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	106	4	US-10-027-725A-10 Sequence 10, Appl1
2	475	87.5	107	4	US-10-016-986-104 Sequence 104, App
3	474	87.3	107	3	US-09-848-798-179 Sequence 179, App
4	474	87.3	107	6	US-11-064-174-179 Sequence 179, App
5	472	86.9	107	3	US-09-848-798-175 Sequence 33, Appl
6	472	86.9	107	3	US-09-848-798-175 Sequence 175, App
7	472	86.9	107	3	US-09-848-798-176 Sequence 176, App
8	472	86.9	107	6	US-11-064-174-176 Sequence 33, Appl
9	472	86.9	107	6	US-11-064-174-175 Sequence 175, App
10	472	86.9	107	6	US-11-064-174-176 Sequence 176, App
11	471	86.7	107	3	US-09-848-798-156 Sequence 156, App
12	471	86.7	107	6	US-11-064-174-156 Sequence 156, App
13	468	86.2	107	3	US-09-848-798-36 Sequence 36, Appl
14	468	86.2	107	6	US-11-064-174-36 Sequence 36, Appl
15	468	86.2	116	5	US-10-783-311-198 Sequence 198, App
16	467	86.0	107	4	US-10-016-986-105 Sequence 105, App
17	465	85.6	111	4	US-10-203-754A-57 Sequence 57, Appl
18	464.5	85.5	108	3	US-09-848-798-32 Sequence 32, Appl
19	464.5	85.5	108	3	US-09-848-798-43 Sequence 43, Appl
20	464.5	85.5	108	6	US-11-064-174-32 Sequence 32, Appl
21	464.5	85.5	108	6	US-11-064-174-43 Sequence 43, Appl
22	464	85.5	107	3	US-09-848-798-37 Sequence 37, Appl
23	464	85.5	107	6	US-11-064-174-37 Sequence 37, Appl
24	464	85.5	108	4	US-10-409-814A-4 Sequence 4, Appl1
25	464	85.5	108	5	US-10-925-366A-3 Sequence 3, Appl1
26	464	85.5	108	5	US-10-925-366A-6 Sequence 6, Appl1
27	464	85.5	108	6	US-11-102-512-3 Sequence 3, Appl1

28	464	85.5	108	6	US-11-102-512-6 Sequence 6, Appl1
29	464	85.5	108	6	US-11-098-758-3 Sequence 3, Appl1
30	464	85.5	108	6	US-11-098-758-6 Sequence 6, Appl1
31	464	85.5	108	6	US-11-166-496-10 Sequence 10, Appl
32	464	85.5	240	3	US-09-192-854-2 Sequence 2, Appl1
33	464	85.5	240	3	US-09-968-561A-2 Sequence 2, Appl1
34	464	85.5	240	3	US-09-968-744A-2 Sequence 2, Appl1
35	464	85.5	240	3	US-09-968-561A-2 Sequence 2, Appl1
36	464	85.5	240	5	US-10-744-774-1 Sequence 1, Appl1
37	464	85.5	240	5	US-10-925-366A-219 Sequence 219, App
38	464	85.5	240	6	US-11-115-682-2 Sequence 2, Appl1
39	464	85.5	240	6	US-11-098-758-219 Sequence 219, App
40	463	85.3	107	3	US-09-791-153A-67 Sequence 67, Appl
41	463	85.3	108	5	US-10-726-332-214 Sequence 214, App
42	463	85.3	108	5	US-10-805-177-64 Sequence 64, Appl
43	462	85.1	106	4	US-10-027-725A-12 Sequence 12, Appl
44	462	85.1	107	3	US-09-848-798-38 Sequence 38, Appl
45	462	85.1	107	3	US-09-848-798-39 Sequence 39, Appl

ALIGNMENTS

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RESULT 1
US-10-027-725A-10
; Sequence 10, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Pickner, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-10

Query Match      100.0%; Score 543; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ELTQSPSSLSASVGRVITISCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
      |||
DB      1  ELTQSPSSLSASVGRVITISCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
QY      61  SSGSGYTDFTLTISLQFEDFASVYQESLSASVYTGQGTKEIKR 106
      |||
DB      61  SSGGYTDFTLTISLQFEDFASVYQESLSASVYTGQGTKEIKR 106

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313,2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
```

;; PRIOR APPLICATION NUMBER: US 08/276,852
;; PRIOR FILING DATE: 1994-07-18
;; PRIOR APPLICATION NUMBER: US 08/178,302
;; PRIOR FILING DATE: 1994-01-06
;; PRIOR APPLICATION NUMBER: PCT/US93/09328
;; PRIOR FILING DATE: 1993-09-30
;; PRIOR APPLICATION NUMBER: US 07/954,148
;; PRIOR FILING DATE: 1992-09-30
;; NUMBER OF SEQ ID NOS: 176
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 104
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match 87.5%; Score 475; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 6.9e-36;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNMYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGDVDTITCRASQISITGLNMYQKPGKAPKLLIYAASSLSQGVPSRF 60
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGQGTVEIKR 106
DB 61 SSGSGYGTDFLTITSSLOPEDFATYTCQOSYSTPTFTFGQGTVEIKR 106

RESULT 3

US-09-848-798-179
;; Sequence 179, Application US/09848798
;; Publication No. US20030040605A1
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-4202
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; CURRENT FILING DATE: 2001-05-04
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 179
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match 87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.5e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNMYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSMSASVGDVDTITCRASQISITGLNMYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGQGTVEIKR 106
DB 62 SSGSGYGTDFLTITSSLOPEDFATYTCQOSYSTPTFTFGQGTVEIKR 107

RESULT 4

US-11-064-174-179
;; Sequence 179, Application US/11064174
;; Publication No. US20050282252A1

;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-4202
;; CURRENT APPLICATION NUMBER: US/11/064,174
;; CURRENT FILING DATE: 2005-02-22
;; PRIOR APPLICATION NUMBER: US/09/240,274
;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: 60/081,380
;; PRIOR FILING DATE: 1998-04-10
;; PRIOR APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 179
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-064-174-179

Query Match 87.3%; Score 474; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.5e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNMYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSMSASVGDVDTITCRASQISITGLNMYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGQGTVEIKR 106
DB 62 SSGSGYGTDFLTITSSLOPEDFATYTCQOSYSTPTFTFGQGTVEIKR 107

RESULT 5

US-09-848-798-33
;; Sequence 33, Application US/09848798
;; Publication No. US20030040605A1
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-4202
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; CURRENT FILING DATE: 2001-05-04
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 33
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match 86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLNMYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVDTITCRASQISITGLNMYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGQGTVEIKR 106
DB 62 SSGSGYGTDFLTITSSLOPEDFATYTCQOSYSTPTFTFGQGTVEIKR 107

```
RESULT 6
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYTDFTLTITSSLPEDFASYCQESLSASYTFGQTKVEIKR 106
DB 62 SSGSGYTDFTLTITSSLPEDFATYCCQSYSTPWTGQTKVEIKR 107

RESULT 7
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYTDFTLTITSSLPEDFASYCQESLSASYTFGQTKVEIKR 106
DB 62 SSGSGYTDFTLTITSSLPEDFATYCCQSYSTPWTGQTKVEIKR 107
```

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DB 62 SSGSGYTDFTLTITSSLPEDFATYCCQSYSTPWTGQTKVEIKR 107

RESULT 8
US-11-064-174-33
; Sequence 33, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-11-064-174-33

Query Match      86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYTDFTLTITSSLPEDFASYCQESLSASYTFGQTKVEIKR 106
DB 62 SSGSGYTDFTLTITSSLPEDFATYCCQSYSTLWTFGQTKVEIKR 107

RESULT 9
US-11-064-174-175
; Sequence 175, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-064-174-175

Query Match      86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
```

```

Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61

Qy 61 SSGSGYGTDFTLTISLQFEDFASYYCOESLSASTYFGQGTKEIKR 106
Db 62 SSGSGGTDFTLTISLQFEDFATYYCOQSYSTPTFTFGQGTKEIKR 107

RESULT 10
US-11-064-174-176
; Sequence 176, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-064-174-176

Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61

Qy 61 SSGSGYGTDFTLTISLQFEDFASYYCOESLSASTYFGQGTKEIKR 106
Db 62 SSGSGGTDFTLTISLQFEDFATYYCOQSYSTPTFTFGQGTKEIKR 107

RESULT 11
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match 86.7%; Score 471; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61

Qy 61 SSGSGYGTDFTLTISLQFEDFASYYCOESLSASTYFGQGTKEIKR 106
Db 62 SSGSGGTDFTLTISLQFEDFATYYCOQSYSTPTFTFGQGTKEIKR 107

RESULT 12
US-11-064-174-156
; Sequence 156, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-064-174-156

Query Match 86.7%; Score 471; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61

Qy 61 SSGSGYGTDFTLTISLQFEDFASYYCOESLSASTYFGQGTKEIKR 106
Db 62 SSGSGGTDFTLTISLQFEDFATYYCOQSYSTPTFTFGQGTKEIKR 107

RESULT 13
US-09-848-798-36
; Sequence 36, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0

```



```
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-848-798-36
```

```
Query Match      86.2%; Score 468; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 3e-35;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60
    |||
DB 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 61
    |||
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGGQTKVEIKR 106
    |||
DB 62 TSGSGGTDFLTITSSLOPEDFATYCCQSYSTRTGTGQTKVEIKR 107
    |||
```

RESULT 14

```
US-11-064-174-36
; Sequence 36, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-11-064-174-36
```

```
Query Match      86.2%; Score 468; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 3e-35;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60
    |||
DB 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 61
    |||
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGGQTKVEIKR 106
    |||
DB 62 TSGSGGTDFLTITSSLOPEDFATYCCQSYSTRTGTGQTKVEIKR 107
    |||
```

RESULT 15

```
US-10-783-311-198
; Sequence 198, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
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; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-198
```

```
Query Match      86.2%; Score 468; DB 5; Length 116;
Best Local Similarity 85.8%; Pred. No. 3.3e-35;
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60
    |||
DB 4 QMTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQHPKAPKLLIYAASSLSQGVPSRF 63
    |||
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGGQTKVEIKR 106
    |||
DB 64 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTRTGTGQTKVEIKR 109
    |||
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Search completed: August 30, 2006, 00:50:40
Job time : 61.7091 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 12.5273 Seconds
(without alignments)
578.960 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543
Sequence: 1 ELTQSPSSISASVGDRTVIS.....QESLSASYFGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US09_NEW_PUB pep.*
- 2: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US08_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US09_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ProdData/2/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474	87.3	107	7	US-11-328-483-179 Sequence 179, App
2	472	86.9	107	7	US-11-328-483-33 Sequence 33, App1
3	472	86.9	107	7	US-11-328-483-175 Sequence 175, App
4	472	86.9	107	7	US-11-328-483-176 Sequence 176, App
5	471	86.7	107	7	US-11-328-483-156 Sequence 156, App
6	468	86.2	106	7	US-11-337-300-41 Sequence 41, App1
7	468	86.2	107	7	US-11-328-483-36 Sequence 36, App1
8	468	86.2	243	7	US-11-337-300-47 Sequence 47, App1
9	468	86.2	244	7	US-11-317-786B-17 Sequence 17, App1
10	468	86.2	244	7	US-11-317-786B-19 Sequence 19, App1
11	468	86.2	245	7	US-11-337-300-51 Sequence 51, App1
12	468	86.2	245	7	US-11-337-300-53 Sequence 53, App1
13	468	86.2	245	7	US-11-337-300-59 Sequence 59, App1
14	468	86.2	245	7	US-11-337-300-63 Sequence 63, App1
15	468	86.2	247	7	US-11-337-300-57 Sequence 57, App1
16	468	86.2	247	7	US-11-337-300-96 Sequence 96, App1
17	468	86.2	248	7	US-11-337-300-61 Sequence 61, App1
18	468	86.2	249	7	US-11-337-300-49 Sequence 49, App1
19	468	86.2	249	7	US-11-337-300-67 Sequence 67, App1
20	468	86.2	249	7	US-11-337-300-69 Sequence 69, App1
21	468	86.2	249	7	US-11-337-300-90 Sequence 90, App1
22	468	86.2	249	7	US-11-337-300-92 Sequence 92, App1
23	464.5	85.5	108	7	US-11-328-483-32 Sequence 32, App1
24	464.5	85.5	108	7	US-11-328-483-43 Sequence 43, App1
25	464	85.5	107	7	US-11-328-483-37 Sequence 37, App1

26	463	85.3	214	7	US-11-337-300-129 Sequence 129, App
27	463	85.3	214	7	US-11-317-786B-13 Sequence 13, App1
28	463	85.3	245	6	US-10-539-402-16 Sequence 16, App1
29	462	85.1	107	7	US-11-328-483-38 Sequence 38, App1
30	462	85.1	107	7	US-11-328-483-39 Sequence 39, App1
31	461	84.9	107	7	US-11-328-483-158 Sequence 158, App
32	460.5	84.8	108	7	US-11-328-483-167 Sequence 167, App
33	459.5	84.6	108	7	US-11-328-483-163 Sequence 163, App
34	459	84.5	109	7	US-11-328-483-163 Sequence 9, App1
35	458	84.3	107	7	US-11-328-483-35 Sequence 35, App1
36	458	84.3	107	7	US-11-328-483-173 Sequence 173, App
37	457	84.2	107	7	US-11-328-483-40 Sequence 40, App1
38	457	84.2	240	7	US-11-317-786B-15 Sequence 15, App1
39	456	84.0	107	7	US-11-328-483-44 Sequence 44, App1
40	455	83.8	107	7	US-11-328-483-103 Sequence 103, App
41	454	83.6	109	7	US-11-094-132-75 Sequence 39, App1
42	453	83.4	105	7	US-11-333-197-52 Sequence 75, App1
43	452	83.2	107	7	US-11-328-483-172 Sequence 52, App1
44	452	83.2	107	7	US-11-328-483-174 Sequence 172, App
45	452	83.2	291	7	US-11-154-103-10 Sequence 10, App1

ALIGNMENTS

RESULT 1
US-11-328-483-179
; Sequence 179, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328, 483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064, 174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240, 274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081, 380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028, 550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-328-483-179
Query Match 87.3%; Score 474; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.5e-37;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
OY 1 ELTQSPSSISASVGDRTVISCRASQRIINTYLMVYQKPGKAPLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSMSASVGDRTVITCRASQSIGTYLMVYQKPGKAPLLIYAASSLSQGVPSRF 61
OY 61 SSGSGVDTFTLTSSLOPEDPASVYQESLSASYTFGQGTKEIKR 106
DB 62 SSGSGDTFTLTSSLOPEDFATVYQOSYSTPMTFGQGTKEIKR 107
RESULT 2
US-11-328-483-33
; Sequence 33, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.

```

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-11-328-483-33

```

```

Query Match          86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 3,8e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

```

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QY 1 ELTQSPSSLSASVGDRTYISCRASQRIINTYINWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2 ELTQSPSSLSASVGDRTYITCRASQSISSYINWYQKPGKAPKLLIYAASSLSQGVPSRF 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 SSGSGGTDFLTITISLQPEDFATYYCOQSYSTMTWTFGGGTVEIKR 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 3
US-11-328-483-175
; Sequence 175, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-328-483-175

```

```

Query Match          86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 3,8e-37;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 ELTQSPSSLSASVGDRTYISCRASQRIINTYINWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2 ELTQSPSSLSASVGDRTYITCRASQSISSYINWYQKPGKAPKLLIYAASSLSQGVPSRF 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 SSGSGGTDFLTITISLQPEDFATYYCOQSYSTMTWTFGGGTVEIKR 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 4
US-11-328-483-176
; Sequence 176, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-328-483-176

```

```

Query Match          86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 3,8e-37;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 ELTQSPSSLSASVGDRTYISCRASQRIINTYINWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2 ELTQSPSSLSASVGDRTYITCRASQSISSYINWYQKPGKAPKLLIYAASSLSQGVPSRF 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 SSGSGYGTDFLTITISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 SSGSGGTDFLTITISLQPEDFATYYCOQSYSTMTWTFGGGTVEIKR 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 5
US-11-328-483-156
; Sequence 156, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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;; CURRENT FILING DATE: 2005-12-22
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 17
;; LENGTH: 244
;; TYPE: PRF
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Amino acid sequence of SC02-378, synthetic
US-11-317-786B-17

Query Match 86.2%; Score 468; DB 7; Length 244;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 136 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 195
QY 61 SSGSGTDFLTITSSLOPEDFASYCOESLSASVTFGCGTKVEIKR 106
DB 196 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 241

RESULT 10
US-11-317-786B-19
; Sequence 19, Application US/11317786B
; Publication No. US2006017451A1
; GENERAL INFORMATION:
; APPLICANT: Van den Oudenrijn, Sonja
; APPLICANT: Bakker, Alexander B.H.
; APPLICANT: Bakker, Adrianus O.
; APPLICANT: Van Melijer, Marja
; TITLE OF INVENTION: BINDING MOLECULES FOR THE TREATMENT OF MYELOID CELL MALIGNANCIES
; FILE REFERENCE: 0090 WO 00 ORD 2578-7546US
; CURRENT APPLICATION NUMBER: US/11/317,786B
; CURRENT FILING DATE: 2005-12-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 244
; TYPE: PRF
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of SC02-161, synthetic
US-11-317-786B-19

Query Match 86.2%; Score 468; DB 7; Length 244;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 136 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 195
QY 61 SSGSGTDFLTITSSLOPEDFASYCOESLSASVTFGCGTKVEIKR 106
DB 196 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 241

RESULT 11
US-11-337-300-51
; Sequence 51, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruijf, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
; FILE REFERENCE: 0091 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/337,300

;; CURRENT FILING DATE: 2006-01-20
;; NUMBER OF SEQ ID NOS: 478
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 51
;; LENGTH: 245
;; TYPE: PRF
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: SC03-003
US-11-337-300-51

Query Match 86.2%; Score 468; DB 7; Length 245;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 137 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 196
QY 61 SSGSGTDFLTITSSLOPEDFASYCOESLSASVTFGCGTKVEIKR 106
DB 197 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 242

RESULT 12
US-11-337-300-53
; Sequence 53, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruijf, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
; FILE REFERENCE: 0091 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/337,300
; CURRENT FILING DATE: 2006-01-20
; NUMBER OF SEQ ID NOS: 478
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 245
; TYPE: PRF
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SC03-005
US-11-337-300-53

Query Match 86.2%; Score 468; DB 7; Length 245;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 137 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 196
QY 61 SSGSGTDFLTITSSLOPEDFASYCOESLSASVTFGCGTKVEIKR 106
DB 197 SSGSGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 242

RESULT 13
US-11-337-300-59
; Sequence 59, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruijf, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
; FILE REFERENCE: 0091 WO 00 ORD

```

; CURRENT APPLICATION NUMBER: US/11/337,300
; CURRENT FILING DATE: 2006-01-20
; NUMBER OF SEQ ID NOS: 478
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 245
; TYPE: PR1
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SC03-008
US-11-337-300-59
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```

Query Match          86.2%; Score 468; DB 7; Length 245;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLQGVPSRF 60
DB 137 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLQGVPSRF 196
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGQGTKEIKR 106
DB 197 SSGSGYGTDFLTITSSLOPEDFATYCCQSYSTPPTFGQGTKEIKR 242
```

RESULT 14

```

US-11-337-300-63
; Sequence 63, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruif, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
; FILE REFERENCE: 0091 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/337,300
; CURRENT FILING DATE: 2006-01-20
; NUMBER OF SEQ ID NOS: 478
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 245
; TYPE: PR1
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SC03-010
US-11-337-300-63
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```

Query Match          86.2%; Score 468; DB 7; Length 245;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
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```

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLQGVPSRF 60
DB 137 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLQGVPSRF 196
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGQGTKEIKR 106
DB 197 SSGSGYGTDFLTITSSLOPEDFATYCCQSYSTPPTFGQGTKEIKR 242
```

RESULT 15

```

US-11-337-300-57
; Sequence 57, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruif, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
```

```

; FILE REFERENCE: 0091 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/337,300
; CURRENT FILING DATE: 2006-01-20
; NUMBER OF SEQ ID NOS: 478
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 247
; TYPE: PR1
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SC03-007
US-11-337-300-57
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Query Match          86.2%; Score 468; DB 7; Length 247;
Best Local Similarity 87.7%; Pred. No. 2.1e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLQGVPSRF 60
DB 139 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLQGVPSRF 198
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGQGTKEIKR 106
DB 199 SSGSGYGTDFLTITSSLOPEDFATYCCQSYSTPPTFGQGTKEIKR 244
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Search completed: August 30, 2006, 00:52:03
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 95.2394 Seconds
(without alignments)
508.875 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547
Sequence: 1 ELTQSPSSLASVGDVRVIT.....QOSYTTLYTFSGSKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	537	98.2	106	5 ABG30449 Abg30449 Human IGE
2	486	88.8	115	10 AEG01347 Aeg01347 Kallikrei
3	484	88.5	107	2 AAR54260 Aar54260 Anti-HIV
4	484	88.5	107	2 AAW01283 Aaw01283 VL region
5	484	88.5	107	3 AAY98244 Aay98244 Anti-gp12
6	484	88.5	107	3 AAY95135 Aay95135 Anti-gp12
7	483	88.3	107	4 AAG33590 Aag33590 Human ant
8	483	88.3	107	6 ABO27397 Abo27397 Anti-Rh(D
9	480	87.8	107	6 AAG33644 Aag33644 Human ant
10	480	87.8	107	6 ABO27451 Abo27451 Anti-Rh(D
11	480	87.8	107	6 ABE74528 Abe74528 Anti-Rh(D
12	478	87.4	115	10 AEG01281 Aeg01281 Kallikrei
13	476	87.0	107	2 AAR54261 Aar54261 Anti-HIV
14	476	87.0	107	2 AAW01284 Aaw01284 VL region
15	476	87.0	107	3 AAY98245 Aay98245 Anti-gp12
16	476	87.0	107	3 AAY95136 Aay95136 Anti-gp12
17	476	87.0	214	10 AEF65410 Aef65410 Anti-Rhd
18	475	86.8	107	4 AAG33663 Aag33663 Human ant
19	475	86.8	107	4 AAG33664 Aag33664 Human ant
20	475	86.8	107	6 ABO27471 Abo27471 Anti-Rh(D
21	475	86.8	107	6 ABO27470 Abo27470 Anti-Rh(D
22	475	86.8	107	10 ABE74547 Abe74547 Anti-Rh(D
23	475	86.8	107	10 ABE74548 Abe74548 Anti-Rh(D

ALIGNMENTS

24	474	86.7	107	4 AAG33667 Aag33667 Human ant
25	474	86.7	107	6 ABO27474 Abo27474 Anti-Rh(D
26	474	86.7	107	10 ABE74653 Abe74653 Anti-Rh(D
27	474	86.7	107	10 ABE74551 Abe74551 Anti-Rh(D
28	474	86.7	214	10 AEF65392 Aef65392 Anti-Rhd
29	473.5	86.6	108	4 AAG33589 Aag33589 Human ant
30	473.5	86.6	108	4 AAG33600 Aag33600 Human ant
31	473.5	86.6	108	6 ABO27407 Abo27407 Anti-Rh(D
32	473.5	86.6	108	6 ABO27396 Abo27396 Anti-Rh(D
33	473.5	86.6	108	6 ABE74415 Abe74415 Anti-Rh(D
34	473.5	86.6	108	10 ABE74404 Abe74404 Anti-Rh(D
35	473	86.5	107	4 AAG33594 Aag33594 Human ant
36	473	86.5	107	6 ABO27401 Abo27401 Anti-Rh(D
37	473	86.5	107	10 ABE74409 Abe74409 Anti-Rh(D
38	473	86.5	109	8 ADP66620 Adp66620 Anti-RAS
39	473	86.5	109	8 ADP66619 Adp66619 Anti-RAS
40	473	86.5	109	8 ADP66623 Adp66623 Anti-RAS
41	473	86.5	109	8 ADO79347 Ado79347 Anti-RAS
42	473	86.5	109	8 ADO79343 Ado79343 Anti-RAS
43	473	86.5	109	8 ADO79344 Ado79344 Anti-RAS
44	473	86.5	111	4 AAG63656 Aag63656 Amino aci
45	473	86.5	111	6 ABj38615 Abj38615 Hepatitis

RESULT 1	ABG30449	standard; protein; 106 AA.
ID	ABG30449	
XX	ABG30449;	
AC	ABG30449;	
XX	21-OCT-2002	(first entry)
DT		
XX	Human IGE Fab clone 60 light chain protein.	
DE		
XX	Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..21
FT		/note= "FRL region"
FT	Region	22..32
FT		/note= "CDR1 region"
FT	Region	33..47
FT		/note= "FR2 region"
FT	Region	48..54
FT		/note= "CDR2 protein"
FT	Region	55..86
FT		/note= "FR3 region"
FT	Region	87..95
FT		/note= "CDR2 region"
FT	Region	96..104
FT		/note= "FR4 region"
FT	Misc-difference	98
FT		/note= "Encoded by CCT"
PN	WO200253595-A1.	
XX	11-JUL-2002.	
PD		
XX	27-DEC-2001; 2001WO-SE002908.	
PF		
XX	29-DEC-2000; 2000SE-00004892.	
PR		
XX	(PHAA) PHARMACIA DIAGNOSTICS AB.	
PA		
XX	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX	WPI; 2002-583604/62.	

DR N-PSDB; ABK69641.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 40; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy, it is also useful for diagnosing a type
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG
CC Fab, clone 60 light chain protein of the invention
XX
SQ Sequence 106 AA:
Query Match 98.2%; Score 537; DB 5; Length 106;
Best Local Similarity 99.1%; Pred. No. 7e-30;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVVTITTCRAPOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITTCRAPOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
QY 61 SSGSGGTEFTLTISNLQFEDPASYYCOQSYTYTYTFGSGTKLEIKR 106
DB 61 SSGSGGTEFTLTISNLQFEDPASYYCOQSYTYTYTFGSGTKLEIKR 106
RESULT 2
AEG01347 standard; protein; 115 AA.
XX
XX AEG01347;
AC
XX 20-APR-2006 (first entry)
DT
XX Kallikrein 1 antibody light chain variable region SEQ ID NO:1174.
DE
XX
KW Antibody, light chain variable region; kallikrein 1; therapeutic;
KW Antiacetabacetic; Respiratory-Gen.; Neuroprotective; Antipneumatic;
KW Antirheumatic; Antiallergic; Osteopathic; Antiallergic;
KW Antinflammatory; Gastrointestinal-Gen.; Antidiabetic; Cytostatic;
KW Cardiovascular-Gen.; utropathic; Angiogenesis inhibitor; asthma;
KW Chronic obstructive pulmonary disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; osteoarthritis; allergic rhinitis; sinusitis;
KW inflammatory bowel disease; diabetes; pancreatitis;
KW interstitial cystitis; neoplasm; pancreatic ductal adenocarcinoma; tumor;
KW angiogenesis; cardiovascular disease.
XX
XX Homo sapiens.
OS
XX WO2006017538-A2.
EN
XX 16-FEB-2006.
PD
XX 03-AUG-2005; 2005WO-US027493.
PF
XX 03-AUG-2004; 2004US-0598506P.
PR 04-OCT-2004; 2004US-0615721P.
XX
XX (DYAX-) DYAX CORP.
PA

XX
XX Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q;
PI
XX WPI, 2006-184027/19.
DR
XX
XX Novel protein comprising immunoglobulin heavy and light chain variable
PT domain sequences, capable of inhibiting human tissue kallikrein-1
PT enzymatic activity, useful for treating human tissue kallikrein-1
PT associated disorder, e.g. asthma.
XX
XX Example; SEQ ID NO 1174; 178pp; English.
PS
XX
XX The invention relates to a protein (I) comprising an immunoglobulin heavy
CC chain (HC) variable domain sequence and an immunoglobulin light chain
CC (LC) variable domain sequence, where the HC variable domain sequence and
CC the LC variable domain sequence form an antigen binding site binding to
CC human tissue kallikrein-1 (hkl) and inhibit enzymatic activity of hkl.
CC Also included is a pharmaceutical composition (II) comprising the protein
CC and carrier. The protein is useful for treating or preventing an hkl
CC associated disorder, which involves administering (I) to a subject to
CC treat or prevent the hkl associated disorder. The disorder is chosen from
CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,
CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,
CC inflammatory bowel diseases, immune mediated diabetes, acute
CC pancreatitis, interstitial cystitis or neoplastic disorder. The disorder
CC is asthma and the asthma is allergic or non-allergic asthma. The disorder
CC or tumor angiogenesis. The method further involves administering a second
CC agent that modulates angiogenesis. The second agent is an anti-vascular
CC endothelial growth factor (VEGF) antibody or its antigen binding
CC fragment. The protein is useful for modulating an hkl activity, for
CC detecting the presence of an hkl protein in vitro, for detecting the
CC presence of an hkl in vivo in a human subject, and for reducing the
CC angiogenesis associated with cardiovascular disorders. The present
CC sequence is the light chain variable region of an anti-kallikrein 1
CC antibody of the invention.
XX
SQ Sequence 115 AA:
Query Match 88.8%; Score 486; DB 10; Length 115;
Best Local Similarity 87.7%; Pred. No. 2.5e-26;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVVTITTCRAPOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 5 QMTQSPSSLSASVGDVVTITTCRAPOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 64
QY 61 SSGSGGTEFTLTISNLQFEDPASYYCOQSYTYTYTFGSGTKLEIKR 106
DB 65 SSGSGGTEFTLTISNLQFEDPASYYCOQSYTYTYTFGSGTKLEIKR 110
RESULT 3
AAR54260 standard; protein; 107 AA.
XX
XX AAR54260;
AC
XX 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
DE
XX Anti-HIV gp120 immunoglobulin light chain variable region b22.
DE
XX
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..21
FT Region /label= PRL
FT Region 22..33

```

FT FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX WO9407922-A1.
XX 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI, 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX diagnosis and for passive immuno-therapy.
XX
XX Claim 5; Page 189; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX using primers specific for heavy and light chain variable regions. The
XX amplification products were inserted into a disclonic vector to produce
XX a library of fragments. E.coli XL1 Blue cells were transformed with the
XX library. Filamentous phage were produced which expressed the MAb regions
XX on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX immunoreactive clones. The light chain VK region sequence AAR54260
XX neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
XX
XX Sequence 107 AA;
SQ
XX
XX Query Match 88.5%; Score 484; DB 2; Length 107;
XX Best Local Similarity 88.7%; Pred. No.3.2e-26;
XX Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 ELTQSPSSLSASVGDRTTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLMWYQKPGKAPKLLIYMASSLSQSGVPSRF 60
XX
XX QY 61 SGGSGGTFTLTISNLOPEDFASYCCOQSYTTLTYTSGSGTKLEIKR 106
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 SGGSGGTFTLTISLQPEDFATYCCOQSYTPTTGTGQTKLEIKR 106
XX
XX Db
XX
XX RESULT 4
XX AAW01283
XX ID AAW01283 standard; protein; 107 AA.
XX
XX AAW01283;
XX
XX 29-JAN-1997 (first entry)
XX
XX VL region of HIV neutralising Mab, clone b22 and B35.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
XX HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX virus infectivity assay; precursor gp160; immunocompetence; human;
XX anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.
XX
XX

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FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX WO9602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI, 1996-179601/18.
XX
XX Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
XX immuno-therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366pp; English.
XX
XX The sequences given in AAW01261-92 represent the light chain variable
XX regions (VL) of a series of monoclonal antibodies (Mab's) which are
XX immunoreactive with HIV glycoprotein gp120 and are capable of
XX neutralising HIV. This sequence represents the sequence of the JX2 gene
XX clones, b22 and B35. A Mab containing this VL sequence has the capacity
XX to reduce HIV infectivity titre in an in vivo virus infectivity assay by
XX 50 % at a concentration of less than 700 ng of antibody/ml, and binds
XX mature gp120 preferentially over the precursor gp160. The Mab may be used
XX for determining immunocompetence of a human anti-HIV antibody and in the
XX detection of HIV infection
XX
XX Sequence 107 AA;
SQ
XX
XX Query Match 88.5%; Score 484; DB 2; Length 107;
XX Best Local Similarity 88.7%; Pred. No.3.2e-26;
XX Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 ELTQSPSSLSASVGDRTTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLMWYQKPGKAPKLLIYMASSLSQSGVPSRF 60
XX
XX QY 61 SGGSGGTFTLTISNLOPEDFASYCCOQSYTTLTYTSGSGTKLEIKR 106
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 SGGSGGTFTLTISLQPEDFATYCCOQSYTPTTGTGQTKLEIKR 106
XX
XX Db
XX
XX RESULT 5
XX AAY98244
XX ID AAY98244 standard; protein; 107 AA.
XX
XX AAY98244;
XX
XX 04-JUL-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX
XX

```

KM passive immunotherapy; reduce severity; HIV-induced disease;
 KM immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU948754-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048754.
 XX
 PR 16-SEP-1999; 99AU-00048754.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 DR WPI; 2000-246867/22.
 XX
 PT Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX

Example 9, Fig 11, 374pp; English.

XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/mL. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 XX Sequence 107 AA;

SO Query Match 88.5%; Score 484; DB 3; Length 107;
 Best Local Similarity 88.7%; Pred. No. 3.2e-26;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106
 DB 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106

RESULT 6

AAV95135
 ID AAV95135 standard; protein; 107 AA.
 XX
 AC AAV95135;
 XX
 DT 30-JUN-2000 (first entry)
 XX
 DE Anti-gp120 antibody light chain variable region from clone b22.
 XX
 KM Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KM reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KM glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 PN AU948756-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-00048756.
 XX
 PR 16-SEP-1999; 99AU-00048756.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 DR WPI; 2000-293393/26.
 XX
 PT Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX

Example 9, Fig 11, 366pp; English.

XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/mL. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX
 XX Sequence 107 AA;

SO Query Match 88.5%; Score 484; DB 3; Length 107;
 Best Local Similarity 88.7%; Pred. No. 3.2e-26;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 QY 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106
 DB 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106

DB 61 SGGSGTDFLTITSLQPEDFATYYCOQSYSTPTFTGGTKLEIKR 106

RESULT 7

AAAG93590
ID AAG93590 standard; protein; 107 AA.

AC AAG93590;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) chain 102 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KM red blood cell; Rh phenotype; diagnosis; therapeutic.

XX Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

(UNPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI: 2001-388931/41.

DR N-PSDB; AAH68647.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in

PT diagnostics requiring a human instead of an animal antibody and in

PT therapeutic medicine.

XX Claim 1; Col 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,

CC preferably a human antibody, (I) having an amino acid sequence comprising

CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has

CC immunostimulant activity and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal

CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH6615 to AAH6726 represent the nucleotide sequence which encode

CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy

CC chain CDR3 amino acid sequences which are given in the exemplification of

CC the present invention

SQ Sequence 107 AA;

Query Match 88.3%; Score 483; DB 4; Length 107;

Best Local Similarity 87.7%; Pred. No. 3.7e-26;

Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

XX 12-SEP-2003 (first entry)

XX Anti-Rh(D) chain 102.

XX Human; Rh(D) binding protein; blood typing; blood product; antibody;

XX magnetically activated cell sorting.

XX Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

(UNPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI: 2003-512273/48.

DR N-PSDB; ACD45311.

PT New human Rh(D)-binding protein useful for various diagnostic and

PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 26; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein

CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence

CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 107 AA;

Query Match 88.3%; Score 483; DB 6; Length 107;

Best Local Similarity 87.7%; Pred. No. 3.7e-26;

Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

DB 61 SGGSGTDFLTITSLQPEDFATYYCOQSYSTPTFTGGTKLEIKR 106

DB 2 ELTQSPSSLSASVGDVVTITCRASQISSTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61

QY 1 ELTQSPSSLSASVGDVVTITCRASQISSTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 60

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH13 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

XX red blood cell; Rh phenotype; diagnosis; therapeutic.

XX Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR WPI; 2001-388931/41.
 DR N-PSDB; AAH68701.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 PS Claim 1; Col 68; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determining the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 4; Length 107;
 Best Local Similarity 87.7%; Pred. No. 6e-26; 4; Indels 0; Gaps 0;
 Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQKPKAPKLLIWSASNLQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQKPKAPKLLIYAASLSRSGVPSRF 61
 QY 61 SSGSGSGTEFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
 DB 62 SSGSGSGTDFLTLTISLQPEDFATYYCOQSYSTPYTFGQGTLEIKR 107

RESULT 10
 ABO27451
 ID ABO27451 standard; protein; 107 AA.
 XX
 AC ABO27451;
 XX
 DT 12-SEP-2003 (first entry)
 XX
 DE Anti-Rh(D) light chain SH13.
 XX
 KM Human; RH(D) binding protein; blood typing; blood product; antibody;
 KM magnetically activated cell sorting.
 XX
 OS Homo sapiens.
 XX
 PN US2003040605-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 04-MAY-2001; 2001US-00848798.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.

XX
 PI Siegel DL;
 XX
 DR WPI; 2003-512273/48.
 DR N-PSDB; ACD45365.
 XX
 PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX
 PS Claim 4; Page 50; 187pp; English.
 XX
 CC The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents the amino acid sequence of a human anti-Rh(D) chain
 XX
 SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 6; Length 107;
 Best Local Similarity 87.7%; Pred. No. 6e-26; 4; Indels 0; Gaps 0;
 Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQKPKAPKLLIWSASNLQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQKPKAPKLLIYAASLSRSGVPSRF 61
 QY 61 SSGSGSGTEFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
 DB 62 SSGSGSGTDFLTLTISLQPEDFATYYCOQSYSTPYTFGQGTLEIKR 107

RESULT 11
 AEE74528
 ID AEE74528 standard; protein; 107 AA.
 XX
 AC AEE74528;
 XX
 DT 23-FEB-2006 (first entry)
 XX
 DE Anti-Rh(D) light chain SH13, SEQ ID 156.
 XX
 KM Rh(D); erythrocyte; tissue typing; transplantation; light chain.
 XX
 OS Synthetic.
 XX
 PN US2005282252-A1.
 XX
 PD 22-DEC-2005.
 XX
 PF 22-FEB-2005; 2005US-00064174.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX
 PA (SIEG/) SIEGEL D L.
 XX
 PI Siegel DL;
 XX
 DR WPI; 2006-046435/05.
 DR N-PSDB; AEE74571.
 XX
 PT New RH(D)-binding proteins, useful for typing donor white blood cells for
 PT human leukocyte antigens for the purposes of matching donors and
 PT recipients for potential transplant matching in the case of both solid
 PT organ or tissue transplanting.
 XX
 PS Claim 5; SEQ ID NO 156; 99pp; English.
 XX
 CC The present invention relates to novel Rh(D) antibody light and heavy
 CC chains. The antibody heavy chains are given in AEE74373-AEE74400 and

CC ABE74511-ABE74525. The antibody light chains are given in ABE74398-
 CC ABE74441 and ABE74526-ABE74553. The Rh(D) antigen is a red blood cell
 CC membrane protein. The antibodies are useful for typing donor white blood
 CC cells for human leukocyte antigen (HLA) antigens for the purposes of
 CC matching donors and recipients for potential transplant matching in the
 CC case of both solid (for example, kidney, heart, liver, lung) and non-
 CC solid (for example, bone marrow) organ or tissue transplanting. The
 CC present sequence is one such antibody light chain.
 XX
 SQ Sequence 107 AA:
 Query Match 87.8%; Score 480; DB 10; Length 107;
 Best Local Similarity 87.7%; Pred. No. 6e-26;
 Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDVVTITTCRARQSIITYLWYQKPGKAPKLLTWSASNLOSQVPSRF 60
 DB 2 ELTQSPSSLSASVGDVVTITTCRASQSISSYLWYQKPGKAPKLLTLYAASLSLQVPSRF 61
 QY 61 SGSGSGTEFTLTITSNLOFEDFASVYCOQSYTTLTYTGGSGTKLEIKR 106
 DB 62 SGSGSGTDFLTITSLQPEDFATYYCOQSYSTLYTGGTKLEIKR 107
 RESULT 12
 ID AEG01281 standard; protein; 115 AA.
 AC AEG01281;
 XX
 DT 20-APR-2006 (first entry)
 XX
 DE Kallikrein 1 antibody light chain variable region SEQ ID NO:1108.
 XX
 KW Antibody; light chain variable region; kallikrein 1; therapeutic;
 KW Antiasthmatic; Respiratory-Gen.; Neuroprotective; Antipsoriatic;
 KW Antirheumatic; Antiarthritic; Osteopathic; Antiasthmatic;
 KW Antiinflammatory; Gastrointestinal-Gen.; Antidiabetic; Cytostatic;
 KW Cardiovascular-Gen.; uropathic; Angiogenesis Inhibitor; asthma;
 KW chronic obstructive pulmonary disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; allergic rhinitis; sinusitis;
 KW inflammatory bowel disease; diabetes; pancreatitis;
 KW interstitial cystitis; neoplasm; pancreatic ductal adenocarcinoma; tumor;
 KW angiogenesis; cardiovascular disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2006017538-A2.
 XX
 PD 16-FEB-2006.
 XX
 PF 03-AUG-2005; 2005WO-US027493.
 XX
 PR 03-AUG-2004; 2004US-0598506P.
 PR 04-OCT-2004; 2004US-0615721P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q;
 XX
 DR WPI; 2006-184027/19.
 XX
 PT Novel protein comprising immunoglobulin heavy and light chain variable
 PT domain sequences, capable of inhibiting human tissue Kallikrein-1
 PT enzymatic activity, useful for treating human tissue Kallikrein-1
 PT associated disorder, e.g. asthma.
 XX
 PS Example; SEQ ID NO 1108; 178pp; English.
 XX
 CC The invention relates to a protein (I) comprising an immunoglobulin heavy
 CC chain (HC) variable domain sequence and an immunoglobulin light chain
 CC (LC) variable domain sequence, where the HC variable domain sequence and
 CC the LC variable domain sequence form an antigen binding site binding to

CC human tissue kallikrein-1 (hK1) and inhibit enzymatic activity of hK1.
 CC Also included is a pharmaceutical composition (II) comprising the protein
 CC and carrier. The protein is useful for treating or preventing an hK1
 CC associated disorder, which involves administering (I) to a subject to
 CC treat or prevent the hK1 associated disorder. The disorder is chosen from
 CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,
 CC inflammatory bowel diseases, immune mediated diabetes, acute
 CC pancreatitis, interstitial cystitis or neoplastic disorder. The disorder
 CC is asthma and the asthma is allergic or non-allergic asthma. The disorder
 CC is a neoplastic disorder, which is metastatic pancreatic adenocarcinoma
 CC or tumor angiogenesis. The method further involves administering a second
 CC agent that modulates angiogenesis. The second agent is an anti-vascular
 CC endothelial growth factor (VEGF) antibody or its antigen binding
 CC fragment. The protein is useful for modulating an hK1 activity, for
 CC detecting the presence of an hK1 protein in vitro, for detecting the
 CC presence of an hK1 in vivo in a human subject, and for reducing the
 CC angiogenesis associated with cardiovascular disorders. The present
 CC sequence is the light chain variable region of an anti-kallikrein 1
 CC antibody of the invention.
 XX
 SQ Sequence 115 AA:
 Query Match 87.4%; Score 478; DB 10; Length 115;
 Best Local Similarity 86.8%; Pred. No. 8.7e-26;
 Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDVVTITTCRARQSIITYLWYQKPGKAPKLLTWSASNLOSQVPSRF 60
 DB 5 QMTQSPSSLSASVGDVVTITTCRASQSISSYLWYQKPGKAPKLLTLYAASLSLQVPSRF 64
 QY 61 SGSGSGTEFTLTITSNLOFEDFASVYCOQSYTTLTYTGGSGTKLEIKR 106
 DB 65 SGSGSGTDFLTITSLQPEDFATYYCOQSYSTLYTGGTKLEIKR 110
 RESULT 13
 ID AAR54261 standard; protein; 107 AA.
 AC AAR54261;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-NOV-1994 (first entry)
 XX
 DE Anti-HIV gp120 immunoglobulin light chain variable region b27.
 XX
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain; variable region;
 KW framework; complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT 49..55
 FT /label= FR2
 FT Region 56..87
 FT /label= CDR2
 FT 88..95
 FT /label= FR3
 FT Region 96..107
 FT /label= CDR3
 FT 108..115
 FT /label= FR4
 XX
 PN WO9407922-A1.
 XX
 PD 14-APR-1994.
 XX

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PF 30-SEP-1993; 93WO-US009328.
XX
PR 30-SEP-1992; 92US-00954148.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 1994-135516/16.
XX
PT New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
PS Claim 5; Page 190; 248pp; English.
XX
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed in the MAb regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAK34261.
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,1e-25;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLNWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLNWYQKPKAPKLLIWAASLQSGVPSRF 60
QY 61 SSGSGSGTEFTLTISNLOFEDFPASYCOQSYTTLTYTSGSKLEIKR 106
DB 61 SSGSGSGTDFLTITISLQPEDFATYCOQSYSTPQTGCGTKLEIKR 106

RESULT 14
AAW01284
ID AAW01284 standard; protein; 107 AA.
XX
AC AAW01284;
XX
DT 29-JAN-1997 (first entry)
XX
DE VL region of HIV neutralising MAb, clone B27.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KM HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KM anti-HIV antibody; detection; HIV infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT Region /label= FR1
FT Region 22..32
FT Region /label= CDR1
FT Region 33..47
FT Region /label= FR2
FT Region 48..54
FT Region /label= CDR2
FT Region 55..86
FT Region /label= FR3
FT Region 87..95
FT Region /label= CDR3
FT Region 96..107
FT Region /label= FR4
XX

```

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PN W09602273-A1.
XX
PD 01-FEB-1996.
XX
PF 11-JUL-1995; 95WO-US008743.
XX
PR 18-JUL-1994; 94US-00276852.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 1996-179601/18.
XX
PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
PT immuno-therapy and detection of HIV infection.
XX
PS Example; Fig 11; 366pp; English.
XX
CC The sequences given in AAW01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAb's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the VK2 gene
CC clone, B27. A MAb containing this VL sequence has the capacity to reduce
CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
CC preferentially over the precursor gp160. The MAb may be used for
CC determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
XX
SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,1e-25;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLNWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLNWYQKPKAPKLLIWAASLQSGVPSRF 60
QY 61 SSGSGSGTEFTLTISNLOFEDFPASYCOQSYTTLTYTSGSKLEIKR 106
DB 61 SSGSGSGTDFLTITISLQPEDFATYCOQSYSTPQTGCGTKLEIKR 106

RESULT 15
AAV98245
ID AAV98245 standard; protein; 107 AA.
XX
AC AAV98245;
XX
DT 04-JUL-2000 (first entry)
XX
DE Anti-gp120 antibody light chain variable region from clone B27.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KM human immunodeficiency virus type 1; HIV-1; infectivity titre;
KM passive immunotherapy; reduce severity; HIV-induced disease;
KM immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT Region /label= FR1
FT Region 22..32
FT Region /label= CDR1
FT Region 33..47
FT Region /label= FR2
FT Region 48..54
FT Region /label= CDR2
FT Region 55..86
FT Region /label= FR3
FT Region 87..95
FT Region /label= CDR3
FT Region 96..107
FT Region /label= FR4
XX
PI Burton DR, Barbas CF, Lerner RA;
XX

```


XX WPI: 2000-246867/22.

DR Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
PT glycoprotein-120.
PS
XX

PS Example 9; Fig 11; 374p; English.

XX This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
CC of reducing an HIV infectivity titre in an in vitro virus infectivity
CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
CC production of the antibody comprises: (a) providing a first
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
CC which does not comprise the sequence represented by AA198206) and a
CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;

Best Local Similarity 87.7%; Pred. No. 1,1e-25; Mismatches 5; Indels 0; Gaps 0;

Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTITTCRAQGISITLYLWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVTITTCRAQGISITLYLWYQKPGKAPKLLIWSASNLQGVPSRF 60
QY 61 SSGSGSTERTLTITSNLQFEDPASYCOQSYTTLTYTSGSGTKLEIKR 106
DB 61 SSGSGSTERTLTITSNLQFEDPASYCOQSYTTLTYTSGSGTKLEIKR 106

Search completed: August 30, 2006, 00:41:46
Job time : 97.2394 sec

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 9.95758 Seconds
(without alignments)
1024.243 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGVDRVTIT.....QOSYTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	85.6	108	2	B49047
2	465	85.0	108	2	S47182
3	465	85.0	127	2	S40367
4	464	84.8	109	2	S31998
5	462	84.5	123	2	S40331
6	457	83.5	122	2	S40370
7	455	83.2	108	2	S44122
8	454	83.0	108	2	S31977
9	453	82.8	129	1	K1H0WK
10	451	82.4	109	2	S31981
11	449	82.1	108	1	K1H0DE
12	447	81.7	108	2	S19674
13	446	81.5	129	2	S40317
14	438	80.1	117	2	S46371
15	437.5	80.0	106	2	PC2624
16	437	79.9	107	2	S36264
17	437	79.9	108	1	K1H0HU
18	437	79.9	120	2	S46370
19	436	79.7	109	2	S31979
20	434	79.3	129	2	S52793
21	433	79.2	128	2	S46372
22	432	79.0	109	2	S31980
23	432	79.0	125	2	S40350
24	431	78.8	109	2	S31982
25	429	78.4	129	2	S52792
26	429	78.4	132	2	S40334
27	428	78.2	109	2	S32001
28	428	78.2	122	2	S40314
29	428	78.2	122	2	S40314

30	428	78.2	132	2	S38646	Ig kappa chain V r
31	427.5	78.2	125	2	S40315	Ig kappa chain - h
32	427	78.1	125	2	S40349	Ig kappa chain V-J
33	425.5	77.8	124	2	S40336	Ig kappa chain V-J
34	424.5	77.6	107	2	S36275	Ig lambda chain V
35	424	77.5	108	1	K1H0U	Ig kappa chain V-I
36	424	77.5	125	2	S40333	Ig kappa chain V-J
37	421.5	77.1	108	2	S30521	Ig kappa chain V r
38	419	76.6	116	2	A27594	Ig kappa chain pre
39	419	76.6	117	2	S24206	Ig kappa chain V r
40	418	76.4	109	2	JN0296	Ig kappa chain V-J
41	418	76.4	129	2	S40369	Ig kappa chain - h
42	417.5	76.3	108	2	S34007	Ig kappa chain V r
43	417	76.2	126	2	S40335	Ig kappa chain V-I
44	416	76.1	108	1	K1H0U	Ig kappa chain V-I
45	416	76.1	108	1	K1H0RE	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #ext_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/References: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UP10000176B44
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:P.113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match 85.6%; Score 468; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 3.8e-34;
Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGVDRVTITCRAROSITRYLMMWQOKPKAPKTLTWSASNTQGVPSRF 60
Db 3 QMTQSPSSLSASVGVDRVTITCRASOSISLYLMMWQOKPKAPKTLTVAASLSQSGVPSRF 62
OY 61 SGSGSGTEFTLTISNLPEDFASVYCOQSYTLTYFGSGTKLEIKR 106
Db 63 SGSGSGTDTLTITSSLPEDFATYCOQSYSTPLTTCGCTKVEIKR 108

RESULT 2

S47182
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 21-Jan-2000
C/Accession: S47182
R/McInosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
Submitted to the EMBL Data Library, June 1994
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A/Reference number: S47181
A/Accession: S47182
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <WCI>
C/Cross-references: UNIPARC:UP10000116185; EMBL:X79786; NID:G506422; PIDD:CA56182.1; PII
C/Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match	85.0%	Score 465	DB 2	Length 108
Best Local Similarity	85.8%	Pred. No. 6.9e-34		
Matches 91	Conservative	9	Mismatches 6	Indels 0
				Gaps 0

QY 1 ELTQSPSPSLASAGVDRPTTICRRAROSTSTYLNMYQOKPGAPPELLTWSASLNQSGVPSRF 60
Db 3 ELTQSPSPSLASAGVDRPTTICRRAROSTSTYLNMYQOKPGAPPELLTWSASLNQSGVPSRF 62
QY 61 SSGSGSGTEFTLLTISNLFQEDFPASYCQOSTYLLYTFGSGTKLEIKR 106
Db 63 SSGSGSGTDFLLTISLQPEDFPATYCCQOSTYITLSGGQRTLEIKR 108
QY

RESULT 3

Ig kappa chain V-J-C region - human
 C|Species: Homo sapiens (man)
 C|Date: 19-May-1994 #sequence _revision 26-May-1995 #text_change 21-Jan-2000
 C|Accession: S40367
 R|Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A|Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A|Reference number: S40312; MUID:94080891; PMID:8258341
 A|Accession: S40367
 A|Status: preliminary; translation not shown
 A|Molecule type: mRNA
 A|Residues: 1-127 <KLE>
 A|Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477
 C|Superfamily: immunoglobulin V region; immunoglobulin homology
 C|Keywords: heterotetramer; immunoglobulin
 C|33-107|Domain: immunoglobulin homology <IM>

Query Match	85.0%;	Score 465;	DB 2;	Length 127;
Best Local Similarly	84.0%;	Pred. No. 8.1e-34;		
Matches 89;	Conservative 11;	Mismatches 6;	Indels 0;	Gaps 0;

```

Qy      1 ELTGSPSSLSASVGDRTVITTCAROSISTYLNWYQQKPKGAPKLLIWSASNLQSGVPSRF 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20 QMTGSPSSLSASVGDRTVITTCAROSISTYLNWYQQKPKGAPKLLIYASLSQSGVPSRF 79

```

Qy	61	SGSGSGTEFTLTISNLOFEDFASYYCQQSYYTLTYFGSGTKLEIKR	106
		: : : : :	
Db	80	SGSGSGTDFTLTISNLOPEDFATYYCQQSINFMTWTFGGTKVEIKR	125

RESULT 4

Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S31998
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McEachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31998
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: UNIPARC:UP10000116497; EMBL:Z15081; NID:Z38501; PIDN:CAA78790.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
C:16-90/Domain: immunoglobulin homology <IM>

Query Match	84.8%;	Score 464;	DB 2;	Length 109;
Best Local Similarity	85.7%;	Pred. No. 8.5e-34;		
Matches 90; Conservative	9;	Mismatches 6;	Indels 0;	Gaps 0;

```

QY      2  LTQSPSSLSASVGDRTVTTCRAQOSISTYLNWYQKPKGAKPKLLIWSASNIQSQVPSRFS  61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4  MTQSPSSLSASVGDRTVTTCRAQOSISAYLNWYQKPKGAKPKLLIYSASSLSQSGVPSRFS  63

```

QY 62 GSGSGTEFTLLISNLQFEDFASYCCQSYTTLVTFGSGTKLEIKR 106

Db

64 GSGSGDTFTLTISLQPEDFATYYCQSYDTPWTFGHGKVEIKR 108

RESULT 5

Ig kappa chain human
 C|Species: Homo sapiens (man)
 C|Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C|Accession: S40331
 R|Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A|Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A|Reference number: S40332; MUID:94080891; PMID:8258341
 A|Accession: S40331
 A|Status: preliminary; translation not shown
 A|Molecule type: mRNA
 A|Residues: 1-123 <KLE>
 A|Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CA55109.1; PIR
 C|Superfamily: immunoglobulin V region; immunoglobulin homology
 C|Keywords: heterocyclamer; immunoglobulin
 F|32-106/Domain: immunoglobulin homology <IMM>

Query Match	84.5%	Score	462	DB 2	Length	123			
Best Local Similarity	84.8%	Pred. No.	1.4e-33						
Matches	89	Conservative	11	Mismatches	5	Indels	0	Gaps	0

```
QY      I ELTQSSLSASVGDRTITTCARQSISTYLNMYQOKPGKAPKLIWSASNLQSGVPSRF 600
      :::::::::::::::::::::::::::::
Db      19 QMTQSSLSASVGDRTITTCASQSISTYLNMYQOKPGKAPKLIYAASSLQSGVPSRF 780
```

```
QY      61  SGGSGTEFTLTISNLQFEDFASYCCQASVTLTYTFGSGTKLEIK 105
      |||||:|||||:| ||||:|||||:| |||||:|
Db      79  SGGSGTDFLTITSSLPEDFATYCCQASVTPRTFGGKTKEIK 123
```

RESULT

Ig kappa chain - human
 C|Species: Homo sapiens (man)
 C|Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C|Accession: S40370
 R|Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A|Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A|Reference number: S40312; WUID:94080891; PMID:8258341
 A|Accession: S40370
 A|Status: preliminary; translation not shown
 A|Molecule type: mRNA
 A|Residues: 1-122 <KLB>
 A|Cross-references: UPI0000116178; EMBL:X72480; NID:9441428; PIDN:CA51148.1; PIR
 C|Superfamily: immunoglobulin V region; immunoglobulin homology
 C|Keywords: heterodimer; immunoglobulin
 F|30-104/Domain: immunoglobulin homology <IMM>

Query Match	83.5%;	Score 457;	DB 2;	Length 122;
Best Local Similarity	84.9%;	Pred. No. 3.5e-33;		
Matches 90; Conservative	8;	Mismatches	8;	Indels 0; Gaps 0;

QY 1 ELTQSSSLASVGDRTITTCARQSIISTYLNWYQKQKPAKLLIWSASNLQSGVPSRF 600
:
Db 17 QLTQSSSLASVGDRTITTCASOSISTFLHWYQONLQKAPKLLIYASNLQSGVPSRF 760

Dy 61 SSGSGTEFTLTISNQFEDFASYYCQSYTTLTYFGSGTKLEIKR 106
|||||:|||||:|||||
Db 77 SSGSGSTDETLTISGLQPEDATVYCCOOSYTPRTFGOGTKVEIKR 122
|||||:|||||:|||||

RESULT

345122
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 24-May-2001

A/Note: the sequence was determined from the differentiated gene

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa chain) disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-22/Domain: signal sequence #Status predicted <SIG>

F/23-109/Product: Ig kappa chain V-I region (Walker) #Status predicted <MAY>

F/23-45/Region: framework 1

F/38-112/Domain: immunoglobulin homology <IMM>

F/46-56/Region: complementarity-determining 1

F/57-71/Region: framework 2

F/72-78/Region: complementarity-determining 2

F/79-110/Region: framework 3

F/111-119/Region: complementarity-determining 3

F/120-129/Region: framework 4

F/45-110/Disulfide bonds: #Status predicted

Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 9,1e-33;
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQGISITLYLNWYQOKPGKAPKLLIWSASNLQGVPSRF 60
Db 25 QMTQSPSSLSASVGDRTVITTCRAQGISITLYLNWYQOKPGKAPKLLIYAASLSQGVTSRF 84

QY 61 GSGSGSTGFLLTITSLNLOFEDPASYYCOQSYTLTYTGSGTKLEIK 105
Db 85 GSGSGSTGFLLTITSLNLOFEDPASYYCOQSYTLTYTGSGTKLEIK 129

RESULT 10

S31981

Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S31981

R/Portlano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLauchlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31981

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <POR>

A/Cross-references: UNIPARC:UPI0000116494; EMBL:Z15077; NID:G38493; PIDD:CAA78786.1; PIDD

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 1.2e-32;
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRAQGISITLYLNWYQOKPGKAPKLLIWSASNLQGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITTCRAQGISITLYLNWYQOKPGKAPKLLIHGASTLESQGVPSRF 63

QY 62 GSGSGSTGFLLTITSLNLOFEDPASYYCOQSYTLTYTGSGTKLEIK 106
Db 64 GSGSGSTGFLLTITSLNLOFEDPASYYCOQSYTLTYTGSGTKLEIK 108

RESULT 11

S31978

Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S31978

R/Portlano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLauchlan, S.M.; Rapoport, B.

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Wed Aug 30 10:03:30 2006

us-10-027-725a-11.rup

Page 1

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 57.8182 Seconds

(without alignments)
1695.862 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547

Sequence: 1 BLTQSPSSLSASVGRVTIT.....QQSYTTLVTFSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	85.4	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
2	465.5	85.1	107	2 Q96S89_HUMAN	Q96S89 homo sapien
3	463	82.8	129	1 KV1B_HUMAN	P04431 homo sapien
4	449	82.1	108	1 KV1B_HUMAN	P01587 homo sapien
5	448.5	82.0	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
6	437	79.9	108	1 KV1H_HUMAN	P01600 homo sapien
7	433	79.2	236	2 Q6GKX8_HUMAN	Q6GKX8 homo sapien
8	431	78.8	236	2 Q6GKX0_HUMAN	Q6GKX0 homo sapien
9	430	78.6	236	2 Q6GKX0_HUMAN	Q6GKX0 homo sapien
10	428	78.2	236	2 Q6PIH7_HUMAN	Q6PIH7 homo sapien
11	424	77.5	108	1 KV1N_HUMAN	P01606 homo sapien
12	423	77.3	234	2 Q72473_HUMAN	Q72473 homo sapien
13	416	76.1	108	1 KV1B_HUMAN	P01594 homo sapien
14	416	76.1	108	1 KV1O_HUMAN	P01607 homo sapien
15	414	75.7	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
16	413.5	75.6	107	1 KV1D_HUMAN	P01596 homo sapien
17	413	75.5	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien
18	412	75.3	129	1 KV1X_HUMAN	P04432 homo sapien
19	411.5	75.2	109	1 KV1T_HUMAN	P01612 homo sapien
20	411	75.1	108	1 KV1S_HUMAN	P01611 homo sapien
21	408	74.6	108	1 KV1V_HUMAN	P04430 homo sapien
22	408	74.6	236	2 Q723Y4_HUMAN	Q723Y4 homo sapien
23	407	74.4	108	1 KV1P_HUMAN	P01598 homo sapien
24	405	74.0	236	2 Q502W4_HUMAN	Q502W4 homo sapien
25	403	73.7	108	1 KV1P_HUMAN	P01608 homo sapien
26	402	73.5	108	1 KV1G_HUMAN	P01593 homo sapien
27	402	73.5	108	1 KV1G_HUMAN	P01599 homo sapien
28	401	73.3	108	1 KV1L_HUMAN	P01604 homo sapien
29	401	73.3	108	1 KV1Y_HUMAN	P80362 homo sapien
30	401	73.3	234	2 Q5EFE6_HUMAN	Q5EFE6 homo sapien
31	401	73.3	236	2 Q6P1T5_HUMAN	Q6P1T5 homo sapien

32	399	72.9	108	1 KV1R_HUMAN	P01610 homo sapien
33	398	72.8	189	2 Q56917_HUMAN	Q56917 homo sapien
34	398	72.8	236	2 Q6GKX9_HUMAN	Q6GKX9 homo sapien
35	397	72.6	244	2 Q65ZC8_HUMAN	Q65ZC8 homo sapien
36	396	72.4	108	1 KV1C_HUMAN	P01595 homo sapien
37	395	72.2	108	1 KV1M_HUMAN	P01605 homo sapien
38	395	72.2	236	2 Q6PIH4_HUMAN	Q6PIH4 homo sapien
39	394	72.0	240	2 Q65ZC9_HUMAN	Q65ZC9 homo sapien
40	393	71.8	108	1 KV1K_HUMAN	P01603 homo sapien
41	384	70.2	108	1 KV1Q_HUMAN	P01609 homo sapien
42	384	70.2	108	1 KV5M_MOUSE	P01646 mus musculu
43	383	70.0	117	1 KV1J_HUMAN	P01602 homo sapien
44	377	68.9	117	1 KV1I_HUMAN	P01601 homo sapien
45	375	68.6	108	1 KV5N_MOUSE	P01647 mus musculu

ALIGNMENTS

RESULT 1
Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
ID Q9UL77_HUMAN
AC Q9UL77;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=92387224; PubMed=151616;
RX Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal strational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autolimmune repertoire";
RT Eur. J. Immunol. 22:2231-2236(1992).
RL [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation";
RT Eur. J. Immunol. 23:391-397(1993).
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC EMBL: AF035037; AAD56273.1; -; mRNA.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSSP: P01607, 1BMW.
DR SMR: Q9UL77; 1-108.
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG V.
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; IG_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.

KM Immunoglobulin domain.
 FT NON_TER 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11738 MM; C06681716C4D16F3 CRC64;
 Query Match 85.4%; Score 467; DB 2; Length 108;
 Best Local Similarity 84.0%; Pred. No. 1,7e-41;
 Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTTTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLGSPVSRF 60
 DB 3 QMTQSPSSLSASVGDRTTTCRASQSISSYLMWYQKPGKAPKLLIWSASNLGSPVSRF 62
 QY 61 SSGSGSGTEFTLTISNLOFEDPASYCOOSYTTLYTFSGGTRKLEIKR 106
 DB 63 SSGSGSGTEFTLTISNLOFEDPASYCOOSYTTLYTFSGGTRKLEIKR 108
 RESULT 2
 ID Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.
 AC Q96SA9; 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.B., Shikman A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mysin
 RT antibody V region genes";
 RL Eur. J. Immunol. 16:12020-2031(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92387224; PubMed=1516616;
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
 RT "Human monoclonal seriatonal autoantibodies isolated from thymic B
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene
 RT segments associated with the autoimmune repertoire";
 RL Eur. J. Immunol. 22:2231-2236(1992).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93170387; PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation";
 RL Eur. J. Immunol. 23:391-397(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
 RA Mahlemer-Lory A., Katz J.B., Pilling M., Gnoesein C., Smith A.,
 RA Diamond B.;
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idiotype";
 RL J. Exp. Med. 174:1639-1652(1991).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91243737; PubMed=1903706;
 RA Blaison G., Kuntz J.L., Pasquali J.L.;
 RT "Molecular analysis of V kappa III variable regions of polyclonal
 RT rheumatoid factors during rheumatoid arthritis";
 RL Eur. J. Immunol. 21:1221-1227(1991).
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 CC EMBL: U96396; AAB68785.1; -, mRNA.
 DR PIR; BA9047; BA9047.
 DR PIR; PH0867; PH0867.
 DR PIR; S16840; S16840.
 DR PIR; S31977; S31977.
 DR PIR; S34083; S34083.
 DR PIR; S34086; S34086.
 DR HSSP; P01607; 1BMW.
 DR SMK; Q96SA9; 1-107.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR Linkhub; Q96SA9; -.
 DR InterPro; IPR003539; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR013106; V-sect.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin domain.
 FT NON_TER 1
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11520 MM; 4B843E9C5B577F16 CRC64;
 Query Match 85.1%; Score 465.5; DB 2; Length 107;
 Best Local Similarity 85.8%; Pred. No. 2.4e-41;
 Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
 QY 1 ELTQSPSSLSASVGDRTTTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLGSPVSRF 60
 DB 3 QMTQSPSSLSASVGDRTTTCRASQSISSYLMWYQKPGKAPKLLIWSASNLGSPVSRF 62
 QY 61 SSGSGSGTEFTLTISNLOFEDPASYCOOSYTTLYTFSGGTRKLEIKR 106
 DB 63 SSGSGSGTEFTLTISNLOFEDPASYCOOSYTTLYTFSGGTRKLEIKR 107
 RESULT 3
 ID K11W HUMAN STANDARD; PRT; 129 AA.
 AC P04431;
 DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
 DT 13-AUG-1987, sequence version 1.
 DT 07-MAR-2006, entry version 39.
 DE Ig kappa chain V-I region Walker precursor.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=85014148; PubMed=6091049;
 RA Klobbeck H.G., Combiato G., Zachau H.G.;
 RT "Immunoglobulin genes of the kappa light chain type from two human
 RT lymphoid cell lines are closely related";
 RL Nucleic Acids Res. 12:6995-7006(1984).
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 CC EMBL: X00965; CA25477.1; ALT_TERM; Genomic DNA.
 DR PIR; A01883; K1HWK.
 DR HSSP; P01607; 1BMW.
 DR SMK; P04431; 23-129.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
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DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT REGION 23 45 /FtId-PRO_0000015170.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 119 Complementarity-determining-3.
FT REGION 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 6.4e-40;
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDRTVITTCRARGISITVLMWYQKPKAKPLIWSASNLQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITTCRARGISITVLMWYQKPKAKPLIWSASNLQSGVPSRF 84
QY 61 SSGSGCTEFTLTISNQLQFEDFASVYCCQSYTYTLTYFGSGTKLEIK 105
DB 85 SSGSGCTDFTLTITSSQLQPEDSATYCCQSYSTLTITFGGTRLEIK 129

RESULT 4
KVLE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig kappa chain V-I region DEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstien C.P., Devernon B.V.;
RL Biochem. J. 123:945-958 (1971).
RT "The amino acid sequence of a human kappa light chain.",
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
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CC -----
CC PIR; A01865; KIHWD.
DR HSSP; P01607; IBMW.
DR SMR; P01597; 4-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006855; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
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FT CHAIN 1 >108 Ig kappa chain V-I region DEB.
FT REGION 1 23 /FtId-PRO_0000059741.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Framework-4.
FT REGION 98 107 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11661 MW; BDB6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.4e-39;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDRTVITTCRARGISITVLMWYQKPKAKPLIWSASNLQSGVPSRF 60
DB 3 ZMTQSPSSLSASVGDRTVITTCRARGISITVLMWYQKPKAKPLIWSASNLQSGVPSRF 62
QY 61 SSGSGCTEFTLTISNQLQFEDFASVYCCQSYTYTLTYFGSGTKLEIK 106
DB 63 SSGSGCTDFTLTITSGLLPEDFATYCCQSYTYTYTFGTRKEMTR 108

RESULT 5
Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.",
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
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CC -----
CC EMBL; AF035033; AAD56269.1; -; mRNA.
DR HSSP; P01607; IBMW.
DR LinkHub; Q9UL81; 1-107.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
FT NON TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 82.0%; Score 448.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.6e-39;
Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTGSPSSLSASVGDRTVITTCRARGISITVLMWYQKPKAKPLIWSASNLQSGVPSRF 60
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Db      3 QMTQSPSSLSASVGDVVTITTCRASQGISISYLNMYQKPGKAPKALLIYAASSLSQGVPSRF 62
QY      61 SSGSGGTEFTLTISNLFQEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
Db      63 SSGSGGTDFTLITISLQPEDFATYYCOQSYAL-TFGPGTKVDIR 107

RESULT 6
KV1H_HUMAN STANDARD; PRT; 108 AA.
ID      KV1H_HUMAN
AC      P01600;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      07-MAR-2006, entry version 44.
DE      Ig kappa chain V-I region Hau.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RX      MEDLINE=71032830; PubMed=4097974;
RA      Watanabe S., Hilschmann N.;
RT      "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT      chain of subgroup I (Bence-Jones protein Hau): subdivision within
RT      subgroups."
RL      Hoppe-Seiler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC      -1- MISCELLANEOUS: This C region of this chain has the INV (3) marker.
CC      -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      PIR; A01868; KIHUHU.
DR      PDB; 1F6L; X-ray; L=1-89.
DR      GO; GO:0005576; C:extracellular region; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      InterPro; IPR013106; V-set.
DR      Pfam; PF07686; V-set; 1.
DR      SMART; SM00409; IG; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG LIKE; 1.
DR      3D-structure; Bence-Jones protein; Direct protein sequencing;
KW      Immunoglobulin domain; Immunoglobulin V region.
FT      CHAIN 1
FT      REGION 1 23 Framework-1.
FT      REGION 24 34 Complementarity-determining-1.
FT      REGION 35 49 Framework-2.
FT      REGION 50 56 Complementarity-determining-2.
FT      REGION 57 88 Framework-3.
FT      REGION 89 97 Complementarity-determining-3.
FT      REGION 98 107 Framework-4.
FT      DISULFID 23 89 By similarity.
FT      NON_TER 108
FT      STRAND 4 7
FT      STRAND 9 12
FT      TURN 15 16
FT      STRAND 19 27
FT      TURN 30 31
FT      STRAND 33 38
FT      TURN 40 41
FT      STRAND 45 49
FT      TURN 50 52
FT      STRAND 53 54
FT      TURN 56 57
FT      TURN 60 61
FT      STRAND 62 67

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FT      TURN 68 69
FT      STRAND 70 75
FT      STRAND 77 77
FT      HELIX 80 82
FT      STRAND 84 90
FT      STRAND 92 95
FT      STRAND 98 98
FT      STRAND 102 105
SQ      SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 2.6e-38;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDVVTITTCRASQGISISYLNMYQKPGKAPKALLIYAASSLSQGVPSRF 60
Db      3 QMTQSPSSLSASVGDVVTITTCRASQGISISYLNMYQKPGKAPKALLIYAASSLSQGVPSRF 62
QY      61 SSGSGGTEFTLTISNLFQEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
Db      63 SSGSGGTDFTLITISLQPEDFATYYCOQNYITPTSGGTREIKR 108

RESULT 7
Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
ID      Q6GMX8_HUMAN
AC      Q6GMX8;
DT      19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT      19-JUL-2004, sequence version 1.
DT      07-FEB-2006, entry version 17.
DE      IGKC protein.
GN      Name=IGKC;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA      Datchenko L., Musina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Heaton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalley D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Primary B-Cells;
RG      NIH MGC Project;
RL      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC      -----
DB      EMBL; BC073764; AAH73764.1; -; mRNA.
DR      SMR; Q6GMX8; 24-235.
DR      Ensembl; ENSG00000163245; Homo sapiens.

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DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR InterPro: IPR013106; V-gel.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGcl; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG-LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8B1AB6559EFC9 CRC64;

Query Match 79.2%; Score 433; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 1.7e-37;
Matches 82; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSIITYLNMVYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITCRARQSIITYLNMVYQKPGKAPKLLIYAAASLQSGVPSRF 84

QY 61 SSGSGGTFTLTISNLOFEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
DB 85 SSGSGGTFTLTISLQPEDFATYCCQASHSPFTFGPGTKVDIKR 130

RESULT 8
Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Green E.D., Dickinson M.C.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Splice;
RC NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC073791; AA073791.1; -; mRNA.
DR SMR; Q6GMW1: 24-236.
DR Ensemble; ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR InterPro: IPR013106; V-gel.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGcl; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG-LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087APAC437 CRC64;

Query Match 78.8%; Score 431; DB 2; Length 236;
Best Local Similarity 79.2%; Pred. No. 2.8e-37;
Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSIITYLNMVYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITCRARQSIITYLNMVYQKPGKAPKLLIYAAASLQSGVPSRF 84

QY 61 SSGSGGTFTLTISNLOFEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
DB 85 SSGSGGTFTLTISLQPEDFATYCCQASHSPFTFGPGTKVDIKR 130

RESULT 9
Q6GMX0_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Splice;
RC Klausner R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
```

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CC      -----
DR      EMBL: BC073775; AAH73775.1; -; mRNA.
DR      SMR; Q6GMX0; 23-236.
DR      Ensembl; ENSG00000163245; Homo sapiens.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      InterPro; IPR013106; V-set.
DR      Pfam; PF07654; C1-set; 1.
DR      SMART; SM00409; IG; 1.
DR      SMART; SM00406; IG; 1.
DR      PROSITE; PS00835; IG-LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR      Hypothetical protein.
KW      SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match      78.6%; Score 430; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 3,6e-37;
Matches 82; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDVVTTCRAAGISITLWVYQOKPKAPKLIMASNLQGVPSRF 60
DB      25 QMTQSPSSLSASVGDVVTTCRAAGISITLWVYQOKPKAPKLIMASNLQGVPSRF 84
QY      61 SSGSGSTFEFTLTISNLOFEDPASVYCOQSYTTLTYTGSGTKLEIKR 106
DB      85 SSGSGSTFEFTLTISNLOFEDPASVYCOQSYTTLTYTGSGTKLEIKR 130

RESULT 10
Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC      Q6PIH7;
DT      05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006, entry version 17.
DE      IGKC protein.
GN      Name=IGKC;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Lung;
RX      MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uedin T.B., Tishiyuki S., Carninci P., Prange C.,
RA      Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

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RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Lung;
RG      NIH MGC Project;
RL      Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL: BC034141; AAH34141.1; -; mRNA.
DR      SMR; P01607; 1A82.
DR      HSSP; P01607; 1A82.
DR      Ensembl; ENSG00000163245; Homo sapiens.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      InterPro; IPR013106; V-set.
DR      Pfam; PF07654; C1-set; *1.
DR      SMART; SM00409; IG; 1.
DR      SMART; SM00406; IG; 1.
DR      PROSITE; PS00835; IG-LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR      SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match      78.2%; Score 428; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 5,9e-37;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDVVTTCRAAGISITLWVYQOKPKAPKLIMASNLQGVPSRF 60
DB      25 QLTQSPSSLSASVGDVVTTCRAAGISITLWVYQOKPKAPKLIMASNLQGVPSRF 84
QY      61 SSGSGSTFEFTLTISNLOFEDPASVYCOQSYTTLTYTGSGTKLEIKR 106
DB      85 SSGSGSTFEFTLTISNLOFEDPASVYCOQSYTTLTYTGSGTKLEIKR 130

RESULT 11
KV1N HUMAN STANDARD; PRT; 108 AA.
ID      KV1N HUMAN
AC      P01606;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      07-MAR-2006, entry version 39.
DE      Ig kappa chain V-1 region OU.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RX      MEDLINE=70201507; PubMed=5447531;
RA      Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT      "Macroglobulin structure: variable sequence of light and heavy
RT      chains.";
RL      Science 169:56-59(1970).
CC      -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC      -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC      macroglobulin.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      PIR; A01872; K1HUOU.
DR      HSSP; P01607; 1BMW.
DR      LinkHub; P01606; -.
DR      GO; GO:0005576; C:extracellular region; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.

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DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >108
FT REGION 1 23 Ig kappa chain V-I region OU.
FT REGION 24 34 /FTID=PRO_0000059748.
FT REGION 35 49 Complementarity-determining-1.
FT REGION 50 56 Framework-2.
FT REGION 57 88 Complementarity-determining-2.
FT REGION 89 97 Framework-3.
FT REGION 98 107 Complementarity-determining-3.
FT REGION 108 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11779 MW; 8283D4A24105827E CRC64;

Query Match 77.5%; Score 424; DB 1; Length 108;
Best Local Similarity 68.3%; Pred. No. 6.3e-37;
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVTTICRARQSIITYLWYQKRGKAPKLLMSASNLQGVPSRF 60
Db 3 QMTZSPSSLSASVGBRTYITTCRASZTISYLBWYZZKPGKAPBLILYAASBLHSGVPSRF 62
QY 61 SGSGSGTEFTLTISNLOFEDFASVYCOQSYTYTLTFGSGTKLEIKR 106
Db 63 SGSGSGTBTFTTISLSLPZBFATYTCZSYSPFTTGZTRLZIKR 108

RESULT 12
ID 072473_HUMAN PRELIMINARY; PRT; 234 AA.
AC 072473;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE IGKC proteain.
GN Homo sapiens (human).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Stropstein M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heaton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Maan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilans D.E.,
RA Schnerch A., Schein U.E., Jones S.U.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RG NIH MGC Project;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC056256; AAH56256.1; -; mRNA.
DR HSSP; P01834; 1HE2.
DR SMR; Q72473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; Igcl; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 234 AA; 35674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.3%; Score 423; DB 2; Length 234;
Best Local Similarity 78.1%; Pred. No. 2e-36;
Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDVTTICRARQSIITYLWYQKRGKAPKLLMSASNLQGVPSRF 61
Db 24 MTQSPSSFSASTDRYITTCRASQSIGSYLWYQKRGKAPKLLMSASNLQGVPSRF 83
QY 62 SGSGSGTEFTLTISNLOFEDFASVYCOQSYTYTLTFGSGTKLEIKR 106
Db 84 GSASGTDFTLTISLCLQSEDFATYCCQYTYTPWTFGTFVEIKR 128

RESULT 13
ID KVI1B_HUMAN STANDARD; PRT; 108 AA.
AC KVI1B_HUMAN
AC P01554;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 46.
DE Ig kappa chain V-I region AU.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.,
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au)." ;
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.,
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au." ;
RL Biophys. Struct. Mech. 1:139-146 (1975).
CC -; MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.

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CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR PIR; A91653; KIHUUV.
DR PDB; 1BW5; X-ray; A/B/C=1-108.
DR PDB; 1JY5; X-ray; A=1-107.
DR Ensemble; ENSG00000173782; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
KW CHAIN
FT 1 >108
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
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FT NON_TER 108 108
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FT TURN 15 16
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FT STRAND 33 38
FT TURN 40 41
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FT TURN 50 52
FT TURN 53 54
FT TURN 56 57
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FT TURN 70 77
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FT STRAND 92 95
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 76.4%; Pred. No. 4.4e-36;
Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSIASVDRVYITTCAROSISTYLNWYQOKRGKAPKLLINSASNLQGVPSRF 60
DB 3 QMTQSPSSLSASVGRVYITTCQASQDLSDYLNWYQOKRGKAPKLLITYDASNLQGVPSRF 62
QY 61 SGGSGGTEFTLLISNLQFEDPASYVCOQSYTLLYFSGSGIKLEIKR 106
DB 63 SGGSGGAHFTTISLSIQPEDLATYVCCQYDYLPMTFPGGTVEIKR 108

RESULT 14
KV10_HUMAN

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ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-UTL-1986, sequence version 1.
DT 07-MAR-2006, entry version 51.
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W.; Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O.; Latman E.B.; Schiffer M.; Huber R.; Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC -----
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DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BW5; X-ray; A/B=1-107.
DR PDB; 1RET; X-ray; A/B=1-107.
DR LinkHub; P01607; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
KW CHAIN
FT 1 >108
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23
FT NON_TER 108 108
FT STRAND 4 7
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FT TURN 15 16
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FT TURN 40 41
FT STRAND 42 42

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FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
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FT TURN 68 69
FT STRAND 70 77
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 92 95
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCEZA CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 4,4e-36;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDVVTITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 62
QY 61 SSGSGSGTEFTLTITSLNQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 63 SSGSGSGTDYFTLTITSLQPEDVATYYCCQYNSAPRTFGPGTKLEIKR 108

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FT NON TER 1 1
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 75.7%; Score 414; DB 2; Length 108;
Best Local Similarity 77.4%; Pred. No. 7.2e-36;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

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QY 61 SSGSGSGTEFTLTITSLNQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 63 SSGSGSGTDYFTLTITSLQPEDVATYYCCQYNSAPRTFGPGTKLEIKR 108

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Job time : 58.8182 secs

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RESULT 15
Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA Manheimer-Lory A., Katz J.B., Pillingner M., Ghosein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idotype.";
RT J. Exp. Med. 174:1639-1652(1991).
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CC
EMBL: AF035044; AAD56280.1; -; mRNA.
DR PIR: PH0863; PH0863.
DR HSSP: P01607; 1BMW.
DR SMR: Q9UL70; 1-108.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG V.
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; IG.1.
DR SMART: SM00406; IG.1.
DR PROSITE: PS50835; IG-LIKE.1.
KW Immunoglobulin domain.

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 14.4545 Seconds
(without alignments)
641.891 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547
Sequence: 1 ELTQSPSSASAVGDRVIT.....QQSYTLTYFGSGTKLKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /EMC_Celerra_SIDS3/prodata/2/1aa/6 COMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/1aa/7 COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/8 COMB.pep:*
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6: /EMC_Celerra_SIDS3/prodata/2/1aa/10 COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/11 COMB.pep:*

Pred. No. is the number of results predicted by chance to a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	88.5	107	1 US-08-276-852-104	Sequence 104, App
2	484	88.5	107	1 US-08-899-575-104	Sequence 104, App
3	484	88.5	107	1 US-08-899-575-104	Sequence 104, App
4	484	88.5	107	5 PCT-US95-08743-104	Sequence 104, App
5	483	88.3	107	2 US-09-240-274-33	Sequence 33, App1
6	483	88.3	107	2 US-09-848-798-33	Sequence 33, App1
7	480	87.8	107	2 US-09-240-274-156	Sequence 156, App
8	480	87.8	107	2 US-09-848-798-156	Sequence 156, App
9	476	87.0	107	1 US-08-276-852-105	Sequence 105, App
10	476	87.0	107	1 US-08-899-575-105	Sequence 105, App
11	476	87.0	107	1 US-08-899-575-105	Sequence 105, App
12	476	87.0	107	5 PCT-US95-08743-105	Sequence 105, App
13	475	86.8	107	2 US-09-240-274-175	Sequence 175, App
14	475	86.8	107	2 US-09-240-274-175	Sequence 175, App
15	475	86.8	107	2 US-09-848-798-175	Sequence 175, App
16	475	86.8	107	2 US-09-848-798-175	Sequence 175, App
17	474	86.7	107	2 US-09-240-274-179	Sequence 179, App
18	474	86.7	107	2 US-09-848-798-179	Sequence 179, App
19	473.5	86.6	108	2 US-09-240-274-32	Sequence 32, App1
20	473.5	86.6	108	2 US-09-240-274-43	Sequence 43, App1
21	473.5	86.6	108	2 US-09-848-798-32	Sequence 32, App1
22	473.5	86.6	108	2 US-09-848-798-43	Sequence 43, App1
23	473	86.5	107	2 US-09-240-274-37	Sequence 37, App1
24	473	86.5	107	2 US-09-848-798-37	Sequence 37, App1
25	472.5	86.4	108	2 US-09-240-274-167	Sequence 167, App
26	472.5	86.4	108	2 US-09-848-798-167	Sequence 167, App

27	472	86.3	107	2 US-09-240-274-38	Sequence 38, App1
28	472	86.3	107	2 US-09-240-274-39	Sequence 39, App1
29	472	86.3	107	2 US-09-240-274-162	Sequence 162, App
30	472	86.3	107	2 US-09-848-798-38	Sequence 38, App1
31	472	86.3	107	2 US-09-848-798-39	Sequence 39, App1
32	472	86.3	107	2 US-09-848-798-162	Sequence 162, App
33	471	86.1	107	2 US-09-240-274-158	Sequence 158, App
34	471	86.1	107	2 US-09-848-798-158	Sequence 158, App
35	469	85.7	107	2 US-09-240-274-44	Sequence 44, App1
36	469	85.7	107	2 US-09-848-798-44	Sequence 44, App1
37	468	85.6	108	1 US-08-379-057-29	Sequence 29, App1
38	467	85.4	240	2 US-09-192-854-2	Sequence 2, App1
39	467	85.4	240	2 US-09-511-939-2	Sequence 2, App1
40	464.5	84.9	108	2 US-09-240-274-163	Sequence 163, App
41	464.5	84.9	108	2 US-09-848-798-163	Sequence 163, App
42	463	84.6	104	1 US-08-276-852-106	Sequence 106, App
43	463	84.6	104	1 US-08-899-575-106	Sequence 106, App
44	463	84.6	104	1 US-08-899-575-106	Sequence 106, App
45	463	84.6	104	5 PCT-US95-08743-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
Sequence 104, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Filting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-104

```

Query Match      88.5%: Score 484; DB 1; Length 107;
Best Local Similarity 88.7%: Pred. No. 2.2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy      1 ELTQSPSSLASVGDVRYITTCRAQOSISTYLNWYQOKRGA PKLLIWSASNLQSGVSRF 60
      |||
Db      1 ELTQSPSSLASVGDVRYITTCRAQOSISTYLNWYQOKRGA PKLLIYAASSLQSGVSRF 60
      |||

Qy      61 SGGSSGTEFTITITINLQPEDPASYYCOOSYTTLYTFSSGTFLEIKR 106
      |||
Db      61 SGGSSGTEFTITITINLQPEDPATYYCOOSYSTPYTFSGTFLEIKR 106
      |||

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESS: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRL452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      88.5%: Score 484; DB 1; Length 107;
Best Local Similarity 88.7%: Pred. No. 2.2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy      1 ELTQSPSSLASVGDVRYITTCRAQOSISTYLNWYQOKRGA PKLLIWSASNLQSGVSRF 60
      |||
Db      1 ELTQSPSSLASVGDVRYITTCRAQOSISTYLNWYQOKRGA PKLLIYAASSLQSGVSRF 60
      |||

```

```

OY      61  SGGSGGTFFLTITSLNLOPDPFASYYCOQSYTTLTYTFSGTKLEIKR 106
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  SGGSGGTDFLTITISLLOPDPFATYYCOQSYSTPTTFGGTKLEIKR 106

RESULT 3
US-08-899-575-104
: Sequence 104, Application US/08899575
: Patent No. 5804440
: GENERAL INFORMATION:
: APPLICANT: Burton, Dennis R
: APPLICANT: Bardas, Carlos F
: APPLICANT: Lerner, Richard A
: TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
: TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
: NUMBER OF SEQUENCES: 170
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
: STREET: Mail Drop 1PC8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/899,575
: FILING DATE: 24-JUL-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/276,852
: FILING DATE: 18-JUL-1994
: APPLICATION NUMBER: US 08/178,302
: FILING DATE: 30-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/954,148
: FILING DATE: 30-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SCR1452P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 104:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 107 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-899-575-104

Query Match      88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 2.2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY      61  SGGSGGTFFLTITSLNLOPDPFASYYCOQSYTTLTYTFSGTKLEIKR 106
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  SGGSGGTDFLTITISLLOPDPFATYYCOQSYSTPTTFGGTKLEIKR 106

RESULT 4
PCT-US95-08743-104

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```
Sequence 104, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-104
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Query Match
Best Local Similarity 88.5%; Score 484; DB 5; Length 107;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
QY 61 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
DB 61 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
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RESULT 5

```
US-09-240-274-33
Sequence 33, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33
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Query Match
Best Local Similarity 88.3%; Score 483; DB 2; Length 107;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 61
QY 61 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
DB 61 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
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```
DB 62 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 107
```

RESULT 6

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US-09-848-798-33
Sequence 33, Application US/09848798
Patent No. 6858719
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33
```

```
Query Match
Best Local Similarity 88.3%; Score 483; DB 2; Length 107;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 61
QY 61 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 106
DB 62 SGGSGTEFTLTISNLOPEDFASYCQOQSYTTLTYFGSGTKLEIKR 107
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RESULT 7

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US-09-240-274-156
Sequence 156, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 156
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156
```

```
Query Match
Best Local Similarity 87.8%; Score 480; DB 2; Length 107;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGVDRVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 61
```

```

QY      61 SSGSGIEFTLTISNLQFEDPASVYCCQSYTTLVTRGSGTKLEIKR 106
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
        62 SSGSGTDFLTLTISLQPEPATVYCCQSYSTPYTFGGTKLEIKR 107
DB

```

RESULT 8
ITS-09-8A

US-09-848-798-156
 / Sequence 156, Application US/09848798
 / Patent No. 6858719
 / GENERAL INFORMATION:
 / APPLICANT: Siegel, Donald L.
 / TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 / TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 / FILE REFERENCE: 09596-4202
 / CURRENT APPLICATION NUMBER: US/09/848,798
 / PRIOR FILING DATE: 2001-05-04
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
 / PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
 / PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
 / NUMBER OF SEQ ID NOS: 224
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 156
 / LENGTH: 107
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: anti-Rh(D) antibody clone SH13
 US-09-848-798-156

Query Match	87.8%	Score 480	DB 2	Length 107
Best Local Similarity	87.7%	Pred. No.	58	3
Matches	93	Conservative	9	Mismatches 4; Indels 0; Gaps 0;
Cy	1	ELTOSPSSLSASVGRVITTCARQSIISRYILNMYQOKCKAPKLLIWSASNLNOSGVPARF	60	
Db	2	ELTOSPSSLSASVGRVITTCARQSIISRYILNMYQOKCKAPKLLIWSASNLNOSGVPARF	61	

```

OY      61 SSGSGTEPLTITISNLQFEDFASYYCQOSYTLTYFGSGTKLEIKR 106
      |||||:|||||:|||||:|||||:|||||
DB      62 SSGSGTDFLTITISSLQPEDFATYYCQOSYSTPYFGGQTKLEIKR 107

```

RESULT 9

US-08-276-852-105
: Sequence 105, Application US/08276852
: Patent No. 5652138
: GENERAL INFORMATION:
: APPLICANT: Burton, Dennis R
: APPLICANT: Barbas, Carlos F
: APPLICANT: Lerner, Richard A
: TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
: TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
: NUMBER OF SEQUENCES: 170
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 NO. 5652138th Torrey Pines Road, Suite 220,
: STREET: Mail Drop TPC8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/276,852
: FILING DATE: 18-JUL-1994
: CLASSIFICATION: 514

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 08/178,302
3 FILING DATE: 30-SEP-1993
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 07/954,148
6 FILING DATE: 30-SEP-1992
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Fitting, Thomas
9 REGISTRATION NUMBER: 34,163
10 REFERENCE/DOCKET NUMBER: SCRI452P
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 619-554-2937
13 TELEFAX: 619-554-6312
14 INFORMATION FOR SEQ ID NO: 105:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 107 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19 MOLECULE TYPE: protein
20
21 US-08-276-852-105

```

Query Match	87.0%;	Score 476;	DB 1;	length 107;
Best Local Similarity	87.7%;	Pred. No.	1.1e-35;	
Matches	93;	Conservative	5;	Mismatches 0; Gaps 0;

Qy	1	ELTQSPSSLSASVSGRVITTCRAPQSIISYLLNMYCOOKPKAPKPLTLWMSAS
Db	1	ELTQSPSSLSASVSGRVITTCRASQSISSYLLNMYCOOKPKAPKPLTLIYASAS
Qy	61	SGSGSGTEFTLTLSNLOFEDFASVYCOQSYTLNLYFGSTKYLEIKR 1066
Db	61	SGSGSGDTFTLTLSLOFEDFATVYCOQSYSPQTFGQTKYLEIKR 1066

RESULT 10

US-08-899-575-105
: Sequence 105, Application US/08899575
: Patent No. 5770440
: GENERAL INFORMATION:
: APPLICANT: Burton, Dennis R
: APPLICANT: Barbac, Carlos P
: APPLICANT: Lerner, Richard A
: TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
: TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
: NUMBER OF SEQUENCES: 170
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
: STREET: Mail Drop TPC8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/899,575
: FILING DATE: 24-JUL-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/276,852
: FILING DATE: 18-JUL-1994
: APPLICATION NUMBER: US 06/178,302
: FILING DATE: 30-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/954,148
: FILING DATE: 30-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Filting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match
Best Local Similarity 87.7%; Score 476; DB 1; Length 107;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITVLMYQOKPGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRARSISITVLMYQOKPGKAPKLLIWSASNLQGVPSRF 60

QY 61 SGSGSGTEFTLTISNLOFEDFASVYCCQSYTTLYTFGSGTKLEIKR 106
DB 61 SGSGSGTEFTLTISNLOFEDFATVYCCQSYSTPOTFGQGTLEIKR 106

RESULT 11
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbae, Carlos F
APPLICANT: Lemner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 NO. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match
Best Local Similarity 87.0%; Score 476; DB 1; Length 107;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITVLMYQOKPGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRARSISITVLMYQOKPGKAPKLLIWSASNLQGVPSRF 60

QY 61 SGSGSGTEFTLTISNLOFEDFASVYCCQSYTTLYTFGSGTKLEIKR 106
DB 61 SGSGSGTEFTLTISNLOFEDFATVYCCQSYSTPOTFGQGTLEIKR 106

RESULT 12
PCT-US95-08743-105
Sequence 105, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match
Best Local Similarity 87.0%; Score 476; DB 5; Length 107;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITVLMYQOKPGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRARSISITVLMYQOKPGKAPKLLIWSASNLQGVPSRF 60

QY 61 SGSGSGTEFTLTISNLOFEDFASVYCCQSYTTLYTFGSGTKLEIKR 106
DB 61 SGSGSGTEFTLTISNLOFEDFATVYCCQSYSTPOTFGQGTLEIKR 106

RESULT 13
US-09-240-274-175
Sequence 175, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11

```
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175
```

```
Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.4e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITCRASQISSYLNWYQOKPGKAPKLLIYAASSLQSGVPSRF 61
```

```
QY 61 SGGSGGTEFTLLTISNLOFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFTLLTISLQPEDFATYYCOOSYSTPWTFGGTKVEIKR 107
```

```
RESULT 14
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176
```

```
Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.4e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITCRASQISSYLNWYQOKPGKAPKLLIYAASSLQSGVPSRF 61
```

```
QY 61 SGGSGGTEFTLLTISNLOFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFTLLTISLQPEDFATYYCOOSYSTPWTFGGTKVEIKR 107
```

```
RESULT 15
US-09-848-798-175
; Sequence 175, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
```

```
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175
```

```
Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.4e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITCRASQISSYLNWYQOKPGKAPKLLIYAASSLQSGVPSRF 61
```

```
QY 61 SGGSGGTEFTLLTISNLOFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFTLLTISLQPEDFATYYCOOSYSTPWTFGGTKVEIKR 107
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Search completed: August 30, 2006, 00:37:08
Job time : 15.4545 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 60.7091 Seconds
(without alignments)
808.788 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547
Sequence: 1 ELTQSPSSISASVGDVITIT.....OOSYTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/Pcdata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/Pcdata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/Pcdata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/Pcdata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/Pcdata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/Pcdata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	547	100.0	106	4	US-10-027-725A-11	Sequence 11, App1
2	484	88.5	107	4	US-10-016-986-104	Sequence 104, App
3	483	88.3	107	3	US-09-848-798-33	Sequence 33, App1
4	483	88.3	107	6	US-11-064-174-33	Sequence 33, App1
5	480	87.8	107	3	US-09-848-798-156	Sequence 156, App
6	480	87.8	107	6	US-11-064-174-156	Sequence 156, App
7	476	87.0	107	4	US-10-016-986-105	Sequence 105, App
8	475	86.8	107	3	US-09-848-798-175	Sequence 175, App
9	475	86.8	107	6	US-11-064-174-175	Sequence 175, App
10	475	86.8	107	6	US-11-064-174-176	Sequence 176, App
11	474	86.7	107	3	US-09-848-798-179	Sequence 179, App
12	474	86.7	107	6	US-11-064-174-179	Sequence 179, App
13	473.5	86.6	108	3	US-09-848-798-32	Sequence 32, App1
14	473.5	86.6	108	3	US-09-848-798-43	Sequence 43, App1
15	473.5	86.6	108	6	US-11-064-174-32	Sequence 32, App1
16	473.5	86.6	108	6	US-11-064-174-33	Sequence 33, App1
17	473.5	86.6	107	3	US-09-848-798-37	Sequence 37, App1
18	473	86.5	107	6	US-11-064-174-37	Sequence 37, App1
19	473	86.5	109	6	US-11-127-932-16	Sequence 16, App1
20	473	86.5	109	6	US-11-127-932-17	Sequence 17, App1
21	473	86.5	109	6	US-11-127-932-20	Sequence 20, App1
22	473	86.5	109	6	US-11-127-932-16	Sequence 16, App1
23	473	86.5	109	6	US-11-127-903-17	Sequence 17, App1
24	473	86.5	109	6	US-11-127-903-20	Sequence 20, App1
25	473	86.5	109	6	US-10-203-754A-57	Sequence 57, App1
26	473	86.5	111	4	US-10-203-754A-57	Sequence 57, App1
27	472.5	86.4	108	3	US-09-848-798-167	Sequence 167, App

28	472.5	86.4	108	6	US-11-064-174-167	Sequence 167, App
29	472	86.3	107	3	US-09-848-798-38	Sequence 38, App1
30	472	86.3	107	3	US-09-848-798-39	Sequence 39, App1
31	472	86.3	107	3	US-09-848-798-162	Sequence 162, App
32	472	86.3	107	6	US-11-064-174-38	Sequence 38, App1
33	472	86.3	107	6	US-11-064-174-39	Sequence 39, App1
34	472	86.3	107	6	US-11-064-174-162	Sequence 162, App
35	472	86.3	116	5	US-10-783-311-198	Sequence 198, App
36	471	86.1	107	3	US-09-848-798-158	Sequence 158, App
37	471	86.1	107	6	US-11-064-174-158	Sequence 158, App
38	470	85.9	157	6	US-11-131-648-27	Sequence 27, App1
39	470	85.9	157	6	US-11-131-648-63	Sequence 63, App1
40	469	85.7	107	3	US-09-848-798-44	Sequence 44, App1
41	469	85.7	107	6	US-11-064-174-44	Sequence 44, App1
42	468	85.6	108	5	US-10-726-332-209	Sequence 209, App
43	468	85.6	111	4	US-10-203-754A-56	Sequence 56, App1
44	467	85.4	108	4	US-10-409-814A-4	Sequence 4, App1
45	467	85.4	108	5	US-10-477-830-90	Sequence 90, App1

ALIGNMENTS

```
RESULT 1
US-10-027-725A-11
; Sequence 11, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-11

Query Match      100.0%; Score 547; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.2e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELTQSPSSISASVGDVITITCRARQISITVLMVYQKPGKAPKLLIWSASNLQGVPSRF 60
      |||
DB      1 ELTQSPSSISASVGDVITITCRARQISITVLMVYQKPGKAPKLLIWSASNLQGVPSRF 60
QY      61 SGSGSTFEPTLTISNLOFEDFASVYCOOSYTLTYFGSGTKLEIKR 106
      |||
DB      61 SGSGSTFEPTLTISNLOFEDFASVYCOOSYTLTYFGSGTKLEIKR 106

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
```

```

; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104
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Query Match      88.5%; Score 484; DB 4; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.3e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
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```

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLWSASNLQGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIYAASLSQGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTLTMTFGGKTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTPTTTFGGKTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 3

```

; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33
```

```

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-34;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
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```

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLWSASNLQGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDVVTITCRAROSISSYLNWYQKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTLTMTFGGKTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTLTMTFGGKTKLEIKR 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 4

```

US-11-064-174-33
; Sequence 33, Application US/11064174
; Publication No. US20050282252A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-11-064-174-33
```

```

Query Match      88.3%; Score 483; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-34;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLWSASNLQGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDVVTITCRAROSISSYLNWYQKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTLTMTFGGKTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTLTMTFGGKTKLEIKR 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 5

```

; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156
```

```

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.9e-34;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
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```

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLWSASNLQGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDVVTITCRAROSISSYLNWYQKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTLTMTFGGKTKLEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFLTITSLQPEDFATYTCQOSYSTPTTTFGGKTKLEIKR 107
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 6
US-11-064-174-156
; Sequence 156, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-064-174-156

Query Match 87.8%; Score 480; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 2,9e-34;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVGVTTTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVGVTTTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRF 61

QY 61 SGSGSGTEFTLTITSNLQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 62 SGSGSGTDFTLTITSSLQPEDFATVYCCQSYSTPTFGGQTKLEIKR 107

RESULT 7
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match 87.0%; Score 476; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 6,5e-34;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVGVTTTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVGVTTTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRF 61

QY 61 SGSGSGTEFTLTITSNLQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 62 SGSGSGTDFTLTITSSLQPEDFATVYCCQSYSTPTFGGQTKLEIKR 106

RESULT 8
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 7,9e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVGVTTTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVGVTTTCRARSISITLWYQKPKAPKLLIWSASNLQSGVPSRF 61

QY 61 SGSGSGTEFTLTITSNLQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 62 SGSGSGTDFTLTITSSLQPEDFATVYCCQSYSTPTFGGQTKLEIKR 107

RESULT 9
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176
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```

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 7.9e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNWYQOKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFGSGTKLEIKR 106
62 SGGSGGTDFTLTISLQPEDFATYCOQSYSTPWTFGQTKVEIKR 107
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RESULT 10

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US-11-064-174-175
; Sequence 175, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
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; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
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; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
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; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
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```

; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
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```

; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 175
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
```

```

US-11-064-174-175
```

```

Query Match      86.8%; Score 475; DB 6; Length 107;
Best Local Similarity 85.8%; Pred. No. 7.9e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNWYQOKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFGSGTKLEIKR 106
62 SGGSGGTDFTLTISLQPEDFATYCOQSYSTPWTFGQTKVEIKR 107
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RESULT 11

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US-11-064-174-176
; Sequence 176, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
```

```

; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
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```

; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
```

```

; PRIOR APPLICATION NUMBER: 60/081,380
```

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; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 176
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
```

```

US-11-064-174-176
```

```

Query Match      86.8%; Score 475; DB 6; Length 107;
Best Local Similarity 85.8%; Pred. No. 7.9e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
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```

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNWYQOKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFGSGTKLEIKR 106
62 SGGSGGTDFTLTISLQPEDFATYCOQSYSTPWTFGQTKVEIKR 107
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RESULT 12

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US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
```

```

; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
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; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
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; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 179
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
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US-09-848-798-179
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Query Match      86.7%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 9.6e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSMSASVGDRTVITTCRARSISGTYLNWYQOKPGKAPKLLIYAASLSQGVPSRF 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFGSGTKLEIKR 106
62 SGGSGGTDFTLTISLQPEDFATYCOQSYSTPWTFGQTKVEIKR 107
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RESULT 13

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US-11-064-174-179
; Sequence 179, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
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;; CURRENT APPLICATION NUMBER: US/11/064,174
;; CURRENT FILING DATE: 2005-02-22
;; PRIOR APPLICATION NUMBER: US/09/240,274
;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: 60/081,380
;; PRIOR FILING DATE: 1998-04-10
;; PRIOR APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 179
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-064-174-179

Query Match 86.7%; Score 474; DB 6; Length 107;
Best Local Similarity 85.8%; Pred. No. 9, 6e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARSISTYLNWYQKPKGAPKLIWASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRARSIGTYLNWYQKPKGAPKLIYAASLSQSGVPSRF 61
QY 61 SSGSGTDEFTLTITSNLQFEDFASYCQOSYTT-LYTFGSGTKLEIKR 106
DB 62 SSGSGTDEFTLTITSNLQFEDFASYCQOSYTPYTFGSGTKLEIKR 107

RESULT 14
US-09-848-798-32

;; Sequence 32, Application US/09848798
;; Publication No. US20030040605A1
;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-4202
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; CURRENT FILING DATE: 2001-05-04
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 32
;; LENGTH: 108
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match 86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1, 1e-33;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVVTITTCRARSISTYLNWYQKPKGAPKLIWASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRARSISSTYLNWYQKPKGAPKLIYAASLSQSGVPSRF 61
QY 61 SSGSGTDEFTLTITSNLQFEDFASYCQOSYTT-LYTFGSGTKLEIKR 106
DB 62 SSGSGTDEFTLTITSNLQFEDFASYCQOSYTPYTFGSGTKLEIKR 108

RESULT 15
US-09-848-798-43
;; Sequence 43, Application US/09848798
;; Publication No. US20030040605A1

;; GENERAL INFORMATION:
;; APPLICANT: Siegel, Donald L.
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;; FILE REFERENCE: 09596-4202
;; CURRENT APPLICATION NUMBER: US/09/848,798
;; CURRENT FILING DATE: 2001-05-04
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;; NUMBER OF SEQ ID NOS: 224
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 43
;; LENGTH: 108
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match 86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1, 1e-33;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVVTITTCRARSISTYLNWYQKPKGAPKLIWASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRARSISSTYLNWYQKPKGAPKLIYAASLSQSGVPSRF 61
QY 61 SSGSGTDEFTLTITSNLQFEDFASYCQOSYTT-LYTFGSGTKLEIKR 106
DB 62 SSGSGTDEFTLTITSNLQFEDFASYCQOSYTPYTFGSGTKLEIKR 108

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 12.5273 Seconds
(without alignments)
578,960 Million cell updates/sec

Title: US-10-027-725a-11
Perfect score: 547
Sequence: 1 ELTQSPSSIASVGDVRVIT.....QOSYTLTYFGSGTKLEIKR 106

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Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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Published Applications AA.New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	88.3	107	US-11-328-483-33	Sequence 33, Appl
2	480	87.8	107	US-11-328-483-156	Sequence 156, App
3	475	86.8	107	US-11-328-483-175	Sequence 175, App
4	475	86.8	107	US-11-328-483-176	Sequence 176, App
5	474	86.7	107	US-11-328-483-179	Sequence 179, Appl
6	473.5	86.6	108	US-11-328-483-32	Sequence 32, Appl
7	473.5	86.6	108	US-11-328-483-43	Sequence 43, Appl
8	473	86.5	107	US-11-328-483-37	Sequence 37, Appl
9	472.5	86.4	108	US-11-328-483-167	Sequence 167, App
10	472	86.3	107	US-11-328-483-38	Sequence 38, Appl
11	472	86.3	107	US-11-328-483-39	Sequence 39, Appl
12	472	86.3	107	US-11-328-483-162	Sequence 162, App
13	471	86.1	106	US-11-337-300-41	Sequence 41, Appl
14	471	86.1	107	US-11-328-483-158	Sequence 158, App
15	471	86.1	107	US-11-337-300-47	Sequence 47, Appl
16	471	86.1	244	US-11-317-786B-17	Sequence 17, Appl
17	471	86.1	244	US-11-317-786B-19	Sequence 19, Appl
18	471	86.1	245	US-11-337-300-51	Sequence 51, Appl
19	471	86.1	245	US-11-337-300-53	Sequence 53, Appl
20	471	86.1	245	US-11-337-300-59	Sequence 59, Appl
21	471	86.1	245	US-11-337-300-63	Sequence 63, Appl
22	471	86.1	247	US-11-337-300-57	Sequence 57, Appl
23	471	86.1	247	US-11-337-300-96	Sequence 96, Appl
24	471	86.1	248	US-11-337-300-61	Sequence 61, Appl
25	471	86.1	249	US-11-337-300-49	Sequence 49, Appl

26	471	86.1	249	7	US-11-337-300-67	Sequence 67, Appl
27	471	86.1	249	7	US-11-337-300-69	Sequence 69, Appl
28	471	86.1	249	7	US-11-337-300-90	Sequence 90, Appl
29	471	86.1	249	7	US-11-337-300-92	Sequence 92, Appl
30	469	85.7	107	7	US-11-328-483-44	Sequence 44, Appl
31	466	85.2	214	7	US-11-337-300-129	Sequence 129, App
32	466	85.2	214	7	US-11-317-786B-13	Sequence 13, Appl
33	465	85.0	240	7	US-11-317-786B-15	Sequence 15, Appl
34	464.5	84.9	108	7	US-11-328-483-163	Sequence 163, App
35	463	84.6	107	7	US-11-375-221-103	Sequence 103, App
36	462	84.5	105	7	US-11-333-197-52	Sequence 52, Appl
37	462	84.5	109	7	US-11-254-679-9	Sequence 9, Appl1
38	461	84.3	245	6	US-10-539-402-16	Sequence 16, Appl
39	459	83.9	107	7	US-11-328-483-168	Sequence 168, App
40	457	83.5	107	7	US-11-328-483-36	Sequence 36, Appl
41	457	83.5	109	7	US-11-094-133-75	Sequence 75, Appl
42	456.5	83.5	108	7	US-11-328-483-41	Sequence 41, Appl
43	456	83.4	107	7	US-11-328-483-173	Sequence 173, App
44	455.5	83.3	105	6	US-10-981-300-24	Sequence 24, Appl
45	454	83.0	107	7	US-11-328-483-40	Sequence 40, Appl

ALIGNMENTS

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RESULT 1
US-11-328-483-33
; Sequence 33, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/328,483
; PRIOR APPLICATION NUMBER: 2006-01-09
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rn(D) chain 102
US-11-328-483-33

Query Match      88.3%; Score 483; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.3e-38;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY      1 ELTQSPSSIASVGDVRVITTCRARGISITVLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
Db      2 ELTQSPSSIASVGDVRVITTCRARGISITVLMWYQKPKAPKLLIWSASNLQSGVPSRF 61
QY      61 SSGSGSTFTLTISNLOFEDFASYQOSYTLTYFGSGTKLEIKR 106
Db      62 SSGSGSTFTLTISNLOFEDFASYQOSYTLTYFGSGTKLEIKR 107

RESULT 2
US-11-328-483-156
; Sequence 156, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
```

```

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; PRIOR FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-328-483-156

```

```

Query Match      87.8%; Score 480; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-37;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      1 ELTQSPSSLSASVGDVVTTCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      2 ELTQSPSSLSASVGDVVTTCRAROSISSYLNWYQOKPGKAPKLLIYAASLSLQSGVPSRF 61
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy      61 SSGSGGTEFTLTISNLQPEDFASYYCCQSYTTLTYFGSGTKLEIKR 106
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      62 SSGSGGTEFTLTISNLQPEDFATYYCCQSYSTPTTFGGTKLEIKR 107
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

RESULT 3
US-11-328-483-175
; Sequence 175, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-328-483-175

```

```

Query Match      86.8%; Score 475; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 4e-37;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      1 ELTQSPSSLSASVGDVVTTCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      2 ELTQSPSSLSASVGDVVTTCRASQISSYLNWYQOKPGKAPKLLIYAASLSLQSGVPSRF 61
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

Qy      61 SSGSGGTEFTLTISNLQPEDFASYYCCQSYTTLTYFGSGTKLEIKR 106
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      62 SSGSGGTEFTLTISNLQPEDFATYYCCQSYSTPTTFGGTKLEIKR 107
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

RESULT 4
US-11-328-483-176
; Sequence 176, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-328-483-176

```

```

Query Match      86.8%; Score 475; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 4e-37;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      1 ELTQSPSSLSASVGDVVTTCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      2 ELTQSPSSLSASVGDVVTTCRASQISSYLNWYQOKPGKAPKLLIYAASLSLQSGVPSRF 61
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy      61 SSGSGGTEFTLTISNLQPEDFASYYCCQSYTTLTYFGSGTKLEIKR 106
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      62 SSGSGGTEFTLTISNLQPEDFATYYCCQSYSTPTTFGGTKLEIKR 107
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

RESULT 5
US-11-328-483-179
; Sequence 179, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```



```

: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
: FILE REFERENCE: 09596-4202
: CURRENT APPLICATION NUMBER: US/11/328,483
: CURRENT FILING DATE: 2006-01-09
: PRIOR APPLICATION NUMBER: US/11/064,174
: PRIOR FILING DATE: 2005-02-22
: PRIOR APPLICATION NUMBER: US/09/240,274
: PRIOR FILING DATE: 1999-01-29
: PRIOR APPLICATION NUMBER: 60/081,380
: PRIOR FILING DATE: 1998-04-10
: PRIOR APPLICATION NUMBER: 60/028,550
: PRIOR FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 167
: LENGTH: 108
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURES:
: OTHER INFORMATION: anti-Rh(D) antibody clone SH34
: US-11-328-483-167

```

Query Match	86.4%	Score 472.5	DB 7	Length 108
Best Local Similarity	87.9%	Pred. No. 6.8e-37		
Matches 94	Conservative 7	Mismatches 5	Indels 1	Gaps 1

Qy	Db
61	2
62	61
63	62
64	63
65	64
66	65
67	66
68	67
69	68
70	69
71	70
72	71
73	72
74	73
75	74
76	75
77	76
78	77
79	78
80	79
81	80
82	81
83	82
84	83
85	84
86	85
87	86
88	87
89	88
90	89
91	90
92	91
93	92
94	93
95	94
96	95
97	96
98	97
99	98
100	99

```

RESULT 10
US-11-328-483-38
; Sequence 38, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 107
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-11-328-483-38

```

Query Match	86.3%	Score 472	DB 7	Length 107
Best local Similarity	86.8%	Pred. No. 7.5e-37		
Matches	92	Mismatches	5	Indels 0
		Gaps	0	
QY	1	ELTGPSSLSASVGRVITTCARQISITFLYLMYQOKPEKAKLLIMASNSQGVPRF	60	

Db 2 ELRQSPESLISASVGRVTITICRASOSISSYLNINYOORPKCAPKLLIIYAASLQSGVSRF 61
Qy 61 SGSSSGTEFLTITSNLOFEDFASYYCOQASTYTLTYGSGKLEIKR 106
Db 62 SGSSSGTDFLTITSSLOPEDFATYYCOQASTYTRTGSGKVEIKR 107

```

RESULT 11
US-11-328-483-39
; Sequence 39, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 108
US-11-328-483-39

```

Query Match	86.3%	Score 472	DB 7	Length 107
Best Local Similarity	86.8%	Pred. No. 7	5e-37	
Matches 92	Conservative	5	Indels 0	Gaps 0

Qy ELTQSPSLASVAGDRTITICRABQISITRYLWVYQOKPKKAPRLILWASNSINQSGVPSRF 60
 Db 2 ELTQSPSLASVAGDRTITICRABQISITRYLWVYQOKPKKAPRLILWASNSINQSGVPSRF 61
 Qy 61 SGGSGGTETFLITSLNLPEDFASVYQOQSITTYLTFTGSGTKLEIKR 106
 Db 62 SGGSGSGTDFLLITSLNLPEDFATRYVQOQSITRTGTGGTKVEIKR 107

```

RESULT 12
US-11-328-483-162
; Sequence 162, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 107
; TYPE: PRT
;

```

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH24
US-11-328-483-162

Query Match
Best Local Similarity 86.3%; Score 472; DB 7; Length 107;
Pred. No. 7.5e-37;
Matches 90; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 61
QY 61 SSGSGTEFTLTITSNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
DB 62 TSSGSGTDFLTITSSLOPEDFATYYCOQSYTTLTYFGSGTKLEIKR 107

RESULT 13

US-11-337-300-41
Sequence 41, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: De Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudemilc, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Variable light chain of SC03-001, SC03-002, SC03-003, SC03-004, S
OTHER INFORMATION: C03-005, SC03-007, SC03-008, SC03-009, SC03-010, SC03-013, SC03-0
OTHER INFORMATION: 14, SC03-016 and SC03-018
US-11-337-300-41

Query Match
Best Local Similarity 86.1%; Score 471; DB 7; Length 106;
Pred. No. 9.2e-37;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
QY 61 SSGSGTEFTLTITSNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
DB 61 SSGSGTDFLTITSSLOPEDFATYYCOQSYTTLTYFGSGTKLEIKR 106

RESULT 14

US-11-328-483-158
Sequence 158, Application US/11328483
Publication No. US20060177440A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/11/328,483
CURRENT FILING DATE: 2006-01-09
PRIOR APPLICATION NUMBER: US/11/064,174
PRIOR FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/240,274
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/081,380

PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 158
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-11-328-483-158

Query Match
Best Local Similarity 86.1%; Score 471; DB 7; Length 107;
Pred. No. 9.3e-37;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 61
QY 61 SSGSGTEFTLTITSNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGTDFLTITSSLOPEDFATYYCOQSYTTLTYFGSGTKLEIKR 107

RESULT 15

US-11-337-300-47
Sequence 47, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: ter Meulen, Jan H.
APPLICANT: De Kruif, Cornelis A.
APPLICANT: van den Brink, Edward N.
APPLICANT: Goudemilc, Jaap
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: SC03-001
US-11-337-300-47

Query Match
Best Local Similarity 86.1%; Score 471; DB 7; Length 243;
Pred. No. 2.2e-36;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 135 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 194
QY 61 SSGSGTEFTLTITSNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
DB 195 SSGSGTDFLTITSSLOPEDFATYYCOQSYTTLTYFGSGTKLEIKR 240

Search completed: August 30, 2006, 00:52:01
Job time: 13.5273 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 95.2394 Seconds
(Without alignments)
508,875 Million cell updates/sec

Title: US-10-027-725A-12

Sequence: 1 ELTQSPSSVSASVGRVTIT.....QQANSPFYTGQSTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	96.0	106	5	ABG30450
2	518	94.4	233	7	ABB03713
3	518	94.4	233	7	ADB72874
4	499	90.9	107	10	AEF11002
5	499	90.9	129	10	AEF11041
6	498	90.7	115	10	AEFG1253
7	493	89.8	107	9	ADY26765
8	493	89.8	115	10	ABG01358
9	491	89.4	107	8	ADP22406
10	491	89.4	129	9	ADZ57711
11	490	89.3	107	10	AEF11030
12	490	89.3	129	10	AEF11044
13	489	89.1	236	9	ADZ57703
14	488	88.9	108	9	AEA41079
15	487	88.7	107	8	ADP22216
16	486	88.5	108	9	AEA41087
17	486	88.5	115	10	AEFG1311
18	485	88.3	107	5	ABB07237
19	485	88.3	107	9	AEA08942
20	485	88.3	249	10	AEF73793
21	485	88.3	223	6	ABJ36940
22	484	88.2	129	9	ADZ57710
23	483	88.0			

24	482	87.8	155	10	AEF94857	Aee94857 Antibody
25	482	87.8	155	10	AEF94834	Aee94834 Antibody
26	482	87.8	234	7	ADM47073	Adm47073 Mouse ant
27	481	87.6	129	9	ADZ57708	Adz57708 Germline
28	480	87.4	107	10	AEF73662	Aee73662 Human rab
29	480	87.4	249	10	AEF73761	Aee73761 Human ant
30	479	87.2	107	7	ADP03922	Adp03922 Murine-ex
31	479	87.2	107	7	ADP03994	Adp03994 Murine-ex
32	478	87.1	107	4	AA665571	Aa665571 Antino aci
33	478	87.1	107	7	ADP03924	Adp03924 Murine-ex
34	478	87.1	107	7	ADP03989	Adp03989 Murine-ex
35	478	87.1	107	7	ADP03921	Adp03921 Murine-ex
36	478	87.1	244	5	ABP45870	Abp45870 Human Bly
37	478	87.1	244	9	ADG96697	Adg96697 Single ch
38	478	87.1	244	9	AED78750	Aed78750 Human B L
39	477	86.9	107	9	ADK15508	Adk15508 Human ant
40	477	86.9	107	9	ADK98404	Adk98404 Human ant
41	477	86.9	129	9	ADK98252	Adk98252 Human ant
42	477	86.9	212	8	ADF76324	Adf76324 M6-L 1lg
43	475.5	86.6	116	10	AEFG1345	Aeg1345 Kallikrei
44	475	86.5	107	10	AEF73646	Aee73646 Human rab
45	475	86.5	236	5	AU74297	Aau74297 Anti-Huma

ALIGNMENTS

RESULT 1	ABG30450	ABG30450 standard; protein; 106 AA.
XX	XX	XX
AC	XX	ABG30450;
XX	XX	21-OCT-2002 (first entry)
DT	XX	Human IGB Fab clone 100 light chain protein.
XX	XX	Human, fab; antiallergic; vaccine; grass pollen; Phi p 2;
XX	KM	timothy grass pollen allergen; passive immunotherapy.
XX	XX	XX
OS	XX	Homo sapiens.
XX	XX	XX
FH	XX	Key
FT	XX	Region
FT	XX	Location/Qualifiers
FT	XX	1..21
FT	XX	/note="FR1 region"
FT	XX	22..32
FT	XX	/note="CDR1 region"
FT	XX	33..47
FT	XX	/note="FR2 region"
FT	XX	48..54
FT	XX	/note="CDR2 protein"
FT	XX	55..86
FT	XX	/note="FR3 region"
FT	XX	87..95
FT	XX	/note="Encoded by TCT"
FT	XX	96..104
FT	XX	/note="CDR2 region"
FT	XX	96..104
FT	XX	/note="FR4 region"
FT	XX	MO200253595-A1.
PN	XX	11-JUL-2002
PD	XX	27-DEC-2001; 2001WO-SE002908.
PF	XX	29-DEC-2000; 2000SE-00004892.
PR	XX	(PHAA) PHARMACIA DIAGNOSTICS AB.
PA	XX	Flicker S, Steinberger P, Kraft D, Valenta R;
PI	XX	WPI; 2002-583604/62.
DR	XX	

DR N-PSDB; ABK69642.
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 41; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phl p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phl p 2. The present sequence represents the human IgG
CC Fab, clone 100 light chain protein of the invention
XX
SQ Sequence 106 AA;
XX
Query Match 96.0%; Score 527; DB 5; Length 106;
Best Local Similarity 97.2%; Pred. No. 8.1e-30;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 ELTQSPSSVSASVGDVYTTTCRASQGISWLMAYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 1 ELTQSPSSVSASVGDVYTTTCRASQGISWLMAYQHOPGKAPKLLIYSASSLSQGVPSRF 60
XX
QY 61 SSGSGYGTDFSLTITSSLOFEDSATYTCOQANSFPTTFCGQTKVEIKR 106
Db 61 SSGSGYGTDFSLTITSSLOFEDSATYTCOQANSFPTTFCGQTKVEIKR 106
XX
RESULT 2
AAB03713
ID AAB03713 standard; protein; 233 AA.
XX
AC AAB03713;
XX
DT 04-OCT-2000 (first entry)
XX
DE Immunoglobulin kappa amino acid sequence fragment.
XX
KW Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW immunoglobulin kappa; Igk.
XX
XX Unidentified.
XX
XX OS
XX US6048704-A.
XX
XX PN
XX 11-APR-2000.
XX
XX PD
XX 07-MAR-1997; 97US-00812586.
XX
XX PF
XX 07-MAR-1996; 96US-0012976P.
XX
XX PR
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX PA
XX Tilson MD;
XX
XX PI
XX WPI; 2000-316895/27.
XX
XX DR
XX Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
XX PT disease is purified from human aortic tissue and binds immunoreactively
XX PT with immunoglobulin.

XX
PS Example 3; Col 29-31; 70pp; English.
XX
CC The present invention relates to an isolated microfibrillar protein of
CC approximately 40kD. The protein is isolated from human aortic tissue and
CC binds immunoreactively with immunoglobulin purified from human abdominal
CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
CC aneurysm-associated antigenic protein (AAP). The protein is capable of
CC forming a disulphide bonded dimer. The protein is immunoreactive with
CC human kappa immunoglobulin. Also included in the invention are
CC recombinantly produced human AAA proteins. AAP shows regions of homology
CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
CC presence of AAA-associated immunoglobulin bound to the human aortic
CC tissue. Antibodies directed against AAP can be used to detect AAA
CC disease. The recombinant protein can be used to induce tolerance to
CC antigenic AAA protein in the subject e.g. human. This sequence represents
CC an immunoglobulin kappa amino acid sequence. The sequence shares homology
CC with the AAP of the invention, it was used to identify and characterise
CC AAP
XX
SQ Sequence 233 AA;
XX
Query Match 94.4%; Score 518; DB 3; Length 233;
Best Local Similarity 96.2%; Pred. No. 6.9e-29;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 ELTQSPSSVSASVGDVYTTTCRASQGISWLMAYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 23 ELTQSPSSVSASVGDVYTTTCRASQGISWLMAYQHOPGKAPKLLIYSASSLSQGVPSRF 82
XX
QY 61 SSGSGYGTDFSLTITSSLOFEDSATYTCOQANSFPTTFCGQTKVEIKR 106
Db 83 SSGSGYGTDFSLTITSSLOFEDSATYTCOQANSFPTTFCGQTKVEIKR 128
XX
RESULT 3
ADB72874
ID ADB72874 standard; protein; 233 AA.
XX
AC ADB72874;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.
XX
XX
XX Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;
KW AAA-associated immunoglobulin 40kDa protein.
XX
XX OS
XX Homo sapiens.
XX
XX PN
XX US6537769-B1.
XX
XX PD
XX 25-MAR-2003.
XX
XX PF
XX 28-MAR-2000; 2000US-00535832.
XX
XX PR
XX 07-MAR-1996; 96US-0012976P.
XX
XX PR
XX 07-MAR-1997; 97US-00812586.
XX
XX PA
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX PI
XX Tilson MD;
XX
XX WPI; 2003-687181/65.
XX
XX DR
XX Purified protein useful in diagnosing abdominal aortic aneurysm disease
XX PT in subject, e.g. human, contains specified amino acids.
XX
XX PS
XX Disclosure; Col 73-74; 67pp; English.
XX
XX The present invention relates to the isolation of a protein approximately

CC 40kDa which is purified from human aortic tissue. The protein is
 CC immunoreactive with abdominal aortic aneurysms (AAA)-associated
 CC immunoglobulin. The protein is useful for diagnosing AAA disease in a
 CC subject, e.g. human, by administering the protein or a composition
 CC comprising the protein. The inventive protein is capable of forming a
 CC disulphide-bonded dimer of 80 kDa. The present sequence of unknown
 CC function is given in the Sequence Listing but is not mentioned elsewhere
 CC in the specification.

XX Sequence 233 AA:

Query Match 94.4%; Score 518; DB 7; Length 233;
 Best Local Similarity 96.2%; Pred. No. 6.9e-29;
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTITTCRASQGISWLAWYQHKGAPKLLIYSSLSQGVPSRF 60
 Db 23 ELTQSPSSVSASVGDRTITTCRASQGISWLAWYQHKGAPKLLIYSSLSQGVPSRF 82

Qy 61 SGSGVGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTKEIKR 106
 Db 83 SGSGSGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTKEIKR 128

RESULT 4
 ID AEF11002 standard; protein; 107 AA.

XX AEF11002;
 XX 09-MAR-2006 (first entry)

DE Human clone 3D8 antibody group I variable light chain region.

XX light chain variable region; monoclonal antibody therapy;
 KW antibody identification; antitoxin; antibody; epitope mapping;
 KM antiidiartheic; antibacterial; antiinflammatory; gastrointestinal disease;
 KM clostridium difficile infection; pseudomembranous colitis; inflammation.

XX Homo sapiens.

OS Key Location/Qualifiers
 FH Region 24..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..97
 FT /label= CDR3

PN US2005287150-A1.

PD 29-DEC-2005.

PF 04-FEB-2005; 2005US-00051453.

PR 06-FEB-2004; 2004US-0542357P.

PR 28-SEP-2004; 2004US-0613854P.

PA (UYMA-) UNITV MASSACHUSETTS.

PA (MEDA-) MEDAREX INC.

PI Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HJ,

PI Lowy I, Mandell R, Molrine D, Thomas WD, Zhang H,

XX WPI; 2006-065655/07.

XX N-PSDB; AEF11033.

XX New human monoclonal antibody or its antigen binding portion that
 PT specifically binds to an exotoxin of Clostridium difficile; useful in
 PT preparing a composition for treating a Clostridium difficile-associated
 PT disorder in a mammal.
 XX Claim 20; SEQ ID NO 4; 98pp; English.

XX The present sequence of the variable light chain (Vkappa) region of a
 CC novel isolated human monoclonal antibody produced by hybridoma clone 3D8
 CC and encoded by the nucleic acid of SEQ ID NO. 35 AEF11033, specifically
 CC binds to toxin A, an exotoxin of Clostridium difficile and is used in the
 CC current invention in a method of treating C. difficile-associated disease
 CC (CDAD) in a subject. The antibody or its antigen binding portion of the
 CC invention inhibits CDAD in vivo. The antibody or its antigen binding
 CC portion protects from or inhibits C. difficile-mediated colitis,
 CC antibiotic-associated colitis, C. difficile-mediated pseudomembranous
 CC colitis (PMC), C. difficile-mediated diarrhea in a subject and inhibits
 CC relapse of C. difficile-mediated disease. The variable light chain region
 CC of the antibody or its antigen-binding portion comprises three
 CC complementarily determining regions (CDRs; SEQ ID Nos. 16-18). The
 CC antibody or its antigen binding portion specifically binds to an epitope
 CC consisting of the C-terminal half of toxin B and the toxin B receptor
 CC domain, between amino acids 1777-2366 of the toxin B receptor domain. The
 CC antibody or its antigen binding portion specifically binds to an epitope
 CC within the C-terminal receptor binding domain of toxin A, between amino
 CC acids 1853-2710 of toxin A. The antibody or its antigen binding portion
 CC specifically binds to toxin A or B with a KD of less than 20 microm. The
 CC antibody or its antigen binding portion comprises a heavy chain variable
 CC region that is the product of or derived from a human VH 3-33 gene and
 CC comprises a light chain variable region that is the product of or derived
 CC from a human Vkappa gene consisting of VK L19, VK L6 or VK L15. The
 CC antibody or its antigen binding portion comprises a heavy chain variable
 CC region that is the product of or derived from a human VH 5-51 gene and
 CC comprises a light chain variable region that is the product of or derived
 CC from a human VK A27 gene. The antibody or its antigen-binding portion
 CC comprises an effector or an Fc domain. The antibody or its antigen-
 CC binding portion is a single-chain antibody or a Fab fragment. The
 CC antibody or its antigen-binding portion is administered in combination
 CC with a second agent. The second agent is a second human monoclonal
 CC antibody or its antigen-binding portion, a C. difficile vaccine, and/or
 CC an antibiotic such as vancomycin or metronidazole. The antibody or
 CC antigen binding portion thereof specifically binds to C. difficile toxin
 CC A and the second human monoclonal antibody or antigen binding portion
 CC thereof specifically binds to Clostridium difficile toxin B.

SO Sequence 107 AA;

Query Match 90.9%; Score 499; DB 10; Length 107;
 Best Local Similarity 91.4%; Pred. No. 7.5e-28;
 Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTITTCRASQGISWLAWYQHKGAPKLLIYSSLSQGVPSRF 60
 Db 3 QMTQSPSSVSASVGDRTITTCRASQGISWLAWYQHKGAPKLLIYSSLSQGVPSRF 62

Qy 61 SGSGVGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTKEIKR 105
 Db 63 SGSGSGTDFSLTISLQPEDPATYCCQANSFPYTFGQGTKEIKR 107

RESULT 5

ID AEF11041 standard; protein; 129 AA.

XX AEF11041;

XX 09-MAR-2006 (first entry)

DE Human clone 3D8 antibody full length group I Vkappa region.

XX light chain variable region; monoclonal antibody therapy;
 KW antibody identification; antitoxin; antibody; epitope mapping;
 KM antiidiartheic; antibacterial; antiinflammatory; gastrointestinal disease;
 KM clostridium difficile infection; pseudomembranous colitis; inflammation.

XX Homo sapiens.

OS Key Location/Qualifiers
 FH Key Peptide 1..22

FT /label= leader_peptide
 FT 23..129
 FT /label= Mature anti-C. difficile toxin A antibody_group_1
 FT /label= variable_light_chain_region
 FT 46..56
 FT /label= CDR1
 FT 72..78
 FT /label= CDR2
 FT 111..119
 FT /label= CDR3
 FT
 FT US2005287150-A1.
 FT
 FT 29-DEC-2005.
 FT
 FT 04-FEB-2005; 2005US-00051453.
 FT
 FT 06-FEB-2004; 2004US-0542357P.
 FT 28-SEP-2004; 2004US-0613854P.
 FT
 FT (UYMA-) UNIV MASSACHUSETTS.
 FT (MEDA-) MEDAREX INC.
 FT
 FT Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HJ;
 FT Lowy I, Mandell R, Molrine D, Thomas WD, Zhang H;
 FT
 FT WPI; 2006-065655/07.
 FT
 FT New human monoclonal antibody or its antigen binding portion that
 FT specifically binds to an exotoxin of Clostridium difficile, useful in
 FT preparing a composition for treating a Clostridium difficile-associated
 FT disorder in a mammal.
 FT
 FT Disclosure; SEQ ID NO 43; 98bp; English.
 FT
 FT
 FT The present full length sequence is that of the variable light chain
 FT (Vkappa) region of a novel isolated human monoclonal antibody produced by
 FT hybridoma clone 3D8 (group I) which specifically binds to toxin A, an
 FT exotoxin of Clostridium difficile, and is used in the current invention
 FT in a method of treating C. difficile-associated disease (CDAD) in a
 FT subject. The antibody or its antigen binding portion of the invention
 FT inhibits CDAD in vivo. The antibody or its antigen binding portion
 FT protects from or inhibits C. difficile-mediated colitis, antibiotic-
 FT associated colitis, C. difficile-mediated pseudomembranous colitis (PMC),
 FT C. difficile-mediated diarrhea in a subject and inhibits release of C.
 FT difficile-mediated disease. The variable light chain region of the
 FT antibody or its antigen-binding portion comprises three complementarity
 FT determining regions (CDRs; SEQ ID NOs. 16-18). The antibody or its
 FT antigen binding portion specifically binds to an epitope consisting of
 FT the C-terminal half of toxin B and the toxin B receptor domain, between
 FT amino acids 1777-2366 of the toxin B receptor domain. The antibody or its
 FT antigen binding portion specifically binds to an epitope within the C-
 FT terminal receptor binding domain of toxin A, between amino acids 1853-
 FT 2710 of toxin A. The antibody or its antigen binding portion specifically
 FT binds to toxin A or B with a KD of less than 20 microm. The antibody or
 FT its antigen binding portion comprises a heavy chain variable region that
 FT is the product of or derived from a human VH 3-33 gene and comprises a
 FT light chain variable region that is the product of or derived from a
 FT human Vkappa gene consisting of VK L19, VK L6 or VK L15. The antibody or
 FT its antigen binding portion comprises a heavy chain variable region that
 FT is the product of or derived from a human VH 5-51 gene and comprises a
 FT light chain variable region that is the product of or derived from a
 FT human VK A27 gene. The antibody or its antigen-binding portion comprises
 FT an effector or an Fc domain. The antibody or its antigen-binding portion
 FT is a single-chain antibody or a Fab fragment. The antibody or its antigen
 FT -binding portion is administered in combination with a second agent. The
 FT second agent is a second human monoclonal antibody or its antigen-binding
 FT portion, a C. difficile vaccine, and/or an antibiotic such as vancomycin
 FT or metronidazole. The antibody or antigen binding portion thereof
 FT specifically binds to C. difficile toxin A and the second human
 FT monoclonal antibody or antigen binding portion thereof specifically binds
 FT to Clostridium difficile toxin B.

SO Sequence 129 AA;
 Query Match 90.9%; Score 499; DB 10; Length 129;
 Best Local Similarity 91.4%; Pred. No. 8.9e-28;
 Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASGVGRVITTCRASQGISSSWLMAYOHQPKAPKLIIYASSLQSGVPSRF 60
 Db 25 QMTQSPSSVSASGVGRVITTCRASQGISSSWLMAYOHQPKAPKLIIYASSLQSGVPSRF 84
 QY 61 SSGSGYCTDPSLTITSSIQFEDSATIYCOQANSFPYTFGQGTKEIK 105
 Db 85 SSGSGCTDPTLTITSSIQPEDFATYCOQANSFPWTFGQGTKEIK 129
 RESULT 6
 AEG01253
 ID AEG01253 standard; protein, 115 AA.
 XX
 AC AEG01253;
 XX
 DT 20-APR-2006 (first entry)
 XX
 XX Kallikrein 1 antibody light chain variable region SEQ ID NO:1080.
 XX
 XX Antibody; light chain variable region; kallikrein 1; therapeutic;
 KW Antiasthmatic; Respiratory-Gen.; Neuroprotective; Antipsoriatic;
 KW Antirheumatic; Antiarthritic; Osteopathic; Anti-allergic;
 KW Antiinflammatory; Gastrointestinal-Gen.; Antidiabetic; Cytostatic;
 KW Cardiovascular-Gen.; uropathic; Angiogenesis Inhibitor; asthma;
 KW chronic obstructive pulmonary disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; allergic rhinitis; sinusitis;
 KW inflammatory bowel disease; diabetes; pancreatitis;
 KW interstitial cystitis; neoplasm; pancreatic ductal adenocarcinoma; tumor;
 KW angiogenesis; cardiovascular disease.
 XX
 XX Homo sapiens.
 OS
 XX WC0206017538-A2.
 XX
 PD 16-FEB-2006.
 XX
 PF 03-AUG-2005; 2005WO-US027493.
 XX
 PR 03-AUG-2004; 2004US-0598506P.
 XX 04-OCT-2004; 2004US-0615721P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q;
 XX
 XX WPI; 2006-184027/19.
 DR
 XX Novel protein comprising immunoglobulin heavy and light chain variable
 FT domain sequences, capable of inhibiting human tissue kallikrein-1
 FT enzymatic activity, useful for treating human tissue kallikrein-1
 FT associated disorder, e.g. asthma.
 FT
 FT Example; SEQ ID NO 1080; 178bp; English.
 PS
 XX The invention relates to a protein (I) comprising an immunoglobulin heavy
 CC chain (HC) variable domain sequence and an immunoglobulin light chain
 CC (LC) variable domain sequence, where the HC variable domain sequence and
 CC the LC variable domain sequence form an antigen binding site binding to
 CC human tissue kallikrein-1 (hKL) and inhibit enzymatic activity of hKL.
 CC Also included is a pharmaceutical composition (II) comprising the protein
 CC and carrier. The protein is useful for treating or preventing an hKL
 CC associated disorder, which involves administering (I) to a subject to
 CC treat or prevent the hKL associated disorder. The disorder is chosen from
 CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,
 CC inflammatory bowel diseases, immune mediated diabetes, acute
 CC pancreatitis, interstitial cystitis or neoplastic disorder. The disorder

cc pharmaceutical composition comprising a pharmaceutical carrier

PT domain sequences, capable of inhibiting human tissue kallikrein-1

XX	Germine antibody LSVK _L Jk1 light chain protein.
DE	
XX	antibody engineering; cytostatic; vulnery; vasotropic; cardiant;
KW	monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;
KW	gastrointestinal ulcer; ischemia; transplant rejection;
KW	myocardial infarction; reperfusion injury; restenosis; angioplasty;
KW	vascular disease; cancer; retinopathy; endometriosis; arthritis;
KW	Alzheimer's disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;
OS	antibody.
XX	
XX	Homo sapiens.
XX	
XX	GB2404660-A.
PD	
XX	09-FEB-2005.
XX	
PF	04-AUG-2004; 2004GB-00017384.
XX	
PR	04-AUG-2003; 2003US-0492432P.
XX	
XX	(PE12) PEIZER PROD INC.
PA	(ABGE-) ABGENIX INC.
XX	
PI	Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL;
PI	Jia X;
XX	
XX	WPI; 2005-145169/16.
XX	
PT	Human monoclonal antibody or antigen-binding portion that specifically
PT	binds to c-Met, useful for treating cancer by inhibiting c-Met or for
PT	promoting tissue regeneration and wound healing by activating c-Met.
XX	
PS	Example 2; SEQ ID NO 20; 128pp; English.
XX	
CC	The invention relates to a human monoclonal antibody (I) or its antigen-
CC	binding portion that specifically binds to c-Met, comprises a heavy chain
CC	having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is
CC	lysine and X4 is threonine, and a light chain having a fully defined
CC	sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both
CC	chains are without a signal sequence. All the sequences are fully defined
CC	in the specification. (I) is useful for the manufacture of a medicament
CC	for treating a hyperproliferative disorder in a subject, where the
CC	antibody or its portion is a c-Met antagonist. (I) is useful for
CC	manufacture of a medicament for promoting wound healing or tissue
CC	regeneration in a subject, where the antibody, antigen-binding portion or
CC	the composition activates c-Met. (I) which has a c-Met agonist activity
CC	is useful in tissue regeneration or wound healing (skin ulcers or gastric
CC	ulcers), or treating ischemia associated with kidney transplant
CC	rejection, for attenuating toxicity associated with cyclosporin treatment
CC	after transplant surgery, for treating myocardial infarction, cardiac
CC	ischemia due to reperfusion injury, restenosis after angioplasty or
CC	vascular diseases. (I) which has a c-Met antagonist activity is useful
CC	for treating cancers of brain, lung, squamous cell, bladder, neck, liver,
CC	prostate, etc., proliferative vitreoretinopathy, proliferative diabetic
CC	retinopathy, endometriosis, and arthritis, for inhibiting plaque
CC	formation in Alzheimer's disease, inhibiting cellular mitogenic
CC	responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas.
CC	(I) is useful for detecting c-Met in a biological sample in vitro or in
CC	vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has
CC	selectivity for c-Met that is at least 100 times greater than their
CC	selectivity for insulin like growth factor I receptor. This sequence
CC	corresponds to the amino acid sequence for a germine antibody light
CC	chain used in the invention.
XX	
SO	Sequence 129 AA;
XX	
Query Match	89.4%; Score 491; DB 9; Length 129;
Best Local Similarity	90.5%; Pred. No. 3.2e-27;
Matches	95; Conservative 6; Mismatches 4; Indels 0; Gaps 0

Db	25	OMTQSPSSVASVSGDVRITTCRASQGISSEWLMWYQOQKGPAPKLITIVYASSLQSGVPSRF	84
Oy	61	SGSGYGTDSPLTISLQFEEDSATYTCQOANSFPYFGQGTVEIK	105
Db	85	SGSGSGTDFLTITISLQPEDFATYTCQOANSFPWTFGGQGTVEIK	129
RESULT 11			
AF11030	ID	AF11030 standard; protein; 107 AA.	
AC	XX	AF11030;	
XX	XX		
DT	09-MAR-2006	(first entry)	
XX	XX		
DE	XX	Human clone 3D8 antibody group IV variable light chain region.	
KW	XX	light chain variable region; monoclonal antibody therapy;	
KW	XX	antibody identification; antitoxin; antibiotic; epitope mapping;	
KW	XX	antidiarrhetic; antibacterial; antiinflammatory; gastrointestinal disease	
KW	XX	Clostridium difficile infection; pseudomembranous colitis; inflammation.	
OS	XX	Homo sapiens.	
XX	XX		
EH	Key	Location/Qualifiers	
FT	Region	24..34	
FT		/label= CDR1	
FT	Region	50..56	
FT		/label= CDR2	
FT	Region	89..97	
FT		/label= CDR3	
XX	XX		
PN	XX	US2005287150-A1.	
XX	XX		
PD	29-DEC-2005.		
XX	XX		
PP	04-FEB-2005; 2005US-00051453.		
XX	XX		
PR	06-FEB-2004; 2004US-0542357P.		
PR	28-SEP-2004; 2004US-0613854P.		
XX	XX		
PA	(JYMA-) UNIV MASSACHUSETTS		
PA	(MEDA-) MEDAREX INC.		
XX	XX		
PI	Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HJ;		
PI	Lowy I, Mandell R, Molrine D, Thomas WD, Zhang H;		
XX	XX		
DR	WPI; 2006-065655/07.		
XX	XX		
PT	XX	New human monoclonal antibody or its antigen binding portion that	
PT	XX	specifically binds to an exotoxin of Clostridium difficile, useful in	
PT	XX	preparing a composition for treating a Clostridium difficile-associated	
PT	XX	disorder in a mammal.	
PS	XX	Disclosure; SEQ ID NO 32; 98pp; English.	
XX	XX		
XX	XX	The present sequence of the variable light chain (V _κ appal) region of a	
CC	XX	novel isolated human monoclonal antibody produced by hybridoma clone 3D8	
CC	XX	specifically binds to toxin A, an exotoxin of Clostridium difficile and	
CC	XX	is used in the current invention in a method of treating C. difficile-	
CC	XX	associated disease (CDAD) in a subject. The antibody or its antigen	
CC	XX	binding portion of the invention inhibits CPAD in vivo. The antibody or	
CC	XX	its antigen binding portion protects from or inhibits C. difficile-	
CC	XX	mediated colitis, antibiotic-associated colitis, C. difficile-mediated	
CC	XX	pseudomembranous colitis (PMC). C. difficile-mediated diarrhea in a	
CC	XX	subject and inhibits relapse of C. difficile-mediated disease. The	
CC	XX	variable light chain region of the antibody or its antigen-binding	
CC	XX	portion comprises three complementarily determining regions (CDRs). The	
CC	XX	antibody or its antigen binding portion specifically binds to an epitope	
CC	XX	consisting of the C-terminal half of toxin B and the toxin B receptor	
CC	XX	domain, between amino acids 1777-2366 of the toxin B receptor domain. The	
CC	XX	antibody or its antigen binding portion specifically binds to an epitope	
CC	XX	within the C-terminal receptor binding domain of toxin A, between amino	

CC acide 1853-2710 of toxin A. The antibody or its antigen binding portion
 CC specifically binds to toxin A or B with a KD of less than 20 microm. The
 CC antibody or its antigen binding portion comprises a heavy chain variable
 CC region that is the product of or derived from a human VH 3-33 gene and
 CC comprises a light chain variable region that is the product of or derived
 CC from a human V kappa gene consisting of VK L19, VK L6 or VK L15. The
 CC antibody or its antigen binding portion comprises a heavy chain variable
 CC region that is the product of or derived from a human VH 5-51 gene and
 CC comprises a light chain variable region that is the product of or derived
 CC from a human VK A27 gene. The antibody or its antigen-binding portion
 CC comprises an effector or an Fc domain. The antibody or its antigen-
 CC binding portion is a single-chain antibody or a Fab fragment. The
 CC antibody or its antigen-binding portion is administered in combination
 CC with a second agent. The second agent is a second human monoclonal
 CC antibody or its antigen-binding portion, a C. difficile vaccine, and/or
 CC an antibiotic such as vancomycin or metronidazole. The antibody or
 CC antigen binding portion thereof specifically binds to C. difficile toxin
 CC A and the second human monoclonal antibody or antigen binding portion
 CC thereof specifically binds to Clostridium difficile toxin B.

SO Sequence 107 AA;

Query Match 89.3%; Score 490; DB 10; Length 107;
 Best Local Similarity 89.5%; Pred. No. 3.2e-27;
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAAYOHQPGKAPKLLIYASASSLOGVPSRF 60
 Db 3 QMTQSPSSVASVGDRTVITCRASQGISWLAAYOHQPGKAPKLLIYASASSLOGVPSRF 62

QY 61 SSGSGYGFDFSLTITSSLOFEDSATYYCOQANSFYTFGGGKVEIK 105
 Db 63 SSGSGYGFDFSLTITSSLOFEDPATYYCOQVNSFYTFGGGKVEIK 107

RESULT 12
 AEF1044
 ID AEF1044 standard; protein; 129 AA.

AC AEF1044;

DT 09-MAR-2006 (first entry)

XX Human clone 3D8 antibody full length group IV V kappa region.

XX light chain variable region; monoclonal antibody therapy;

KW antibody identification; antitoxin; antibiotic; epitope mapping;
 KW antidiarrheic; antibacterial; antinflammatory; gastrointestinal disease;
 KW Clostridium difficile infection; pseudomembranous colitis; inflammation.

OS Homo sapiens.

XX Location/Qualifiers

FT Key 1..22

FT Peptide /label= leader_peptide

FT Protein 23..129

FT /label= Mature anti-C. difficile_toxin_A_antibody_group_I

FT Region 46..56

FT /label= CDR1

FT Region 72..78

FT /label= CDR2

FT Region 111..119

FT /label= CDR3

XX US2005287150-A1.

XX 29-DEC-2005.

XX 04-FEB-2005; 2005US-00051453.

XX 06-FEB-2004; 2004US-0542357P.

XX 28-SEP-2004; 2004US-0613854P.

XX (UYMA-) UNIV MASSACHUSETTS.
 PA (MEDA-) MEDAREX INC.
 PI Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HU;
 PI Lowy I, Mandell R, Moline D, Thomas WD, Zhang H;
 DR WPI; 2006-065655/07.

XX New human monoclonal antibody or its antigen binding portion that
 PT specifically binds to an exotoxin of Clostridium difficile, useful in
 PT preparing a composition for treating a Clostridium difficile-associated
 PT disorder in a mammal.

PS Disclosure; SEQ ID NO 46; 98pp; English.

XX The present full length sequence is that of the variable light chain
 CC (V kappa) region of a novel isolated human monoclonal antibody produced by
 CC hybridoma clone 308 (group IV) which specifically binds to toxin A, an
 CC exotoxin of Clostridium difficile, and is used in the current invention
 CC in a method of treating C. difficile-associated disease (CDAD) in a
 CC subject. The antibody or its antigen binding portion of the invention
 CC inhibits CDAD in vivo. The antibody or its antigen binding portion
 CC protects from or inhibits C. difficile-mediated pseudomembranous colitis (PMC),
 CC associated colitis, C. difficile-mediated pseudomembranous colitis (PMC),
 CC C. difficile-mediated diarrhea in a subject and inhibits relapse of C.
 CC C. difficile-mediated disease. The variable light chain region of the
 CC antibody or its antigen-binding portion comprises three complementarity
 CC determining regions (CDRs). The antibody or its antigen binding portion
 CC specifically binds to an epitope consisting of the C-terminal half of
 CC toxin B and the toxin B receptor domain, between amino acids 1777-2266 of
 CC the toxin B receptor domain. The antibody or its antigen binding portion
 CC specifically binds to an epitope within the C-terminal receptor binding
 CC domain of toxin A, between amino acids 1853-2710 of toxin A. The antibody
 CC or its antigen binding portion specifically binds to toxin A or B with a
 CC KD of less than 20 microm. The antibody or its antigen binding portion
 CC comprises a heavy chain variable region that is the product of or derived
 CC from a human VH 3-33 gene and comprises a light chain variable region
 CC that is the product of or derived from a human V kappa gene consisting of
 CC VK L19, VK L6 or VK L15. The antibody or its antigen binding portion
 CC comprises a heavy chain variable region that is the product of or derived
 CC from a human VH 5-51 gene and comprises a light chain variable region
 CC that is the product of or derived from a human VK A27 gene. The antibody
 CC or its antigen-binding portion comprises an effector or an Fc domain. The
 CC antibody or its antigen-binding portion is a single-chain antibody or a
 CC Fab fragment. The antibody or its antigen-binding portion is administered
 CC in combination with a second agent. The second agent is a second human
 CC monoclonal antibody or its antigen-binding portion, a C. difficile
 CC vaccine, and/or an antibiotic such as vancomycin or metronidazole. The
 CC antibody or antigen binding portion thereof specifically binds to C.
 CC C. difficile toxin A and the second human monoclonal antibody or antigen
 CC binding portion thereof specifically binds to Clostridium difficile toxin
 CC B.

XX Sequence 129 AA;

Query Match 89.3%; Score 490; DB 10; Length 129;
 Best Local Similarity 89.5%; Pred. No. 3.8e-27;
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAAYOHQPGKAPKLLIYASASSLOGVPSRF 60

Db 25 QMTQSPSSVASVGDRTVITCRASQGISWLAAYOHQPGKAPKLLIYASASSLOGVPSRF 84

QY 61 SSGSGYGFDFSLTITSSLOFEDSATYYCOQANSFYTFGGGKVEIK 105

Db 85 SSGSGYGFDFSLTITSSLOFEDPATYYCOQVNSFYTFGGGKVEIK 129

RESULT 13
 AD257703
 ID AD257703 standard; protein; 236 AA.

AC ADZ57703;
XX
XX 30-JUN-2005 (first entry)
XX
XX Anti-cMet antibody 8.70.2 light chain protein.
XX
XX antibody engineering; cytostatic; vulnery; vasotropic; cardiant;
XX monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;
XX gastrointestinal ulcer; ischemia; transplant rejection;
XX myocardial infarction; reperfusion injury; restenosis; angioplasty;
XX vascular disease; cancer; retinopathy; endometriosis; arthritis;
XX Alzheimer's disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;
XX antibody.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..22
XX /note= "signal peptide"
XX Protein 23..236
XX /note= "mature antibody 8.70.2 light chain protein"
XX Region 46..56
XX /note= "complementarity determining region 1"
XX Region 72..78
XX /note= "complementarity determining region 2"
XX Region 111..119
XX /note= "complementarity determining region 3"
XX
XX GB2404660-A.
XX
XX 09-FEB-2005.
XX
XX 04-AUG-2004; 2004GB-00017384.
XX
XX 04-AUG-2003; 2003US-0492432P.
XX
XX (PF12) PFIZER PROD INC.
XX (ABGE-) ABGENIX INC.
XX
XX Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL,
XX Jia X;
XX
XX MPI; 2005-145169/16.
XX N-PSDB; ADZ57702.
XX
XX
XX Human monoclonal antibody or antigen-binding portion that specifically
XX binds to c-Met, useful for treating cancer by inhibiting c-Met or for
XX promoting tissue regeneration and wound healing by activating c-Met.
XX
XX Claim 6; SEQ ID NO 12; 128pp; English.
XX
XX The invention relates to a human monoclonal antibody (I) or its antigen-
XX binding portion that specifically binds to c-Met, comprises a heavy chain
XX having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is
XX lysine and X4 is threonine, and a light chain having a fully defined
XX sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both
XX chains are without a signal sequence. All the sequences are fully defined
XX in the specification. (I) is useful for the manufacture of a medicament
XX for treating a hyperproliferative disorder in a subject, where the
XX antibody or its portion is a c-Met antagonist. (I) is useful for
XX manufacture of a medicament for promoting wound healing or tissue
XX regeneration in a subject, where the antibody, antigen-binding portion or
XX the composition in a subject, where the antibody, antigen-binding portion or
XX is useful in tissue regeneration or wound healing (skin ulcers or gastric
XX ulcers), or treating ischemia associated with kidney transplant
XX rejection, for attenuating toxicity associated with cyclosporin treatment
XX after transplant surgery, for treating myocardial infarction, cardiac
XX ischemia due to reperfusion injury, restenosis after angioplasty or
XX vascular diseases (I) which has a c-Met antagonist activity is useful
XX for treating cancers of brain, lung, squamous cell, bladder, neck, liver,
XX prostate, etc., proliferative vitreoretinopathy, proliferative diabetic
XX retinopathy, endometriosis, and arthritis, for inhibiting plaque
XX formation in Alzheimer's disease, inhibiting cellular mitogenic

CC responses, or for treating tumor, glioblastoma, sarcoma, or carcinomas.
CC (I) is useful for detecting c-Met in a biological sample in vitro or in
CC vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has
CC selectivity for c-Met that is at least 100 times greater than their
CC selectivity for insulin like growth factor I receptor. This sequence
CC corresponds to the antibody 8.70.2 light chain used in the invention.
XX
XX Sequence 236 AA;
SQ
Query Match 89.1%; Score 489; DB 9; Length 236;
Best Local Similarity 89.6%; Pred. No. 7, 6e-27;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGVDRVTITCRASOGISWLAAYQHQPAPKPLTIYSASLSQGVPSRF 60
DB 25 QMTQSPSSVSASVGVDRVTITCRASOGISWLAAYQHQPAPKPLTIYSASLSQGVPSRF 84
QY 61 SSGSGGTDFSLTISLQFEDSATYCYCOANSPFYFGCGTXYEIKR 106
DB 85 SSGSGGTDFSLTISLQFEDSATYCYCOANSPFYFGCGTXYEIKR 130
RESULT 14
AEA41079
ID AEA41079 standard; protein; 108 AA.
XX
XX AEA41079;
AC
XX
XX 28-JUL-2005 (first entry)
XX
XX Germline V kappa L5, J kappa 3 amino acid sequence SEQ ID NO:109.
XX
XX monoclonal antibody; macrophage colony stimulating factor inhibition;
XX light chain.
XX
XX Unidentified.
XX
XX GB2405873-A.
XX
XX 16-MAR-2005.
XX
XX 09-SEP-2004; 2004GB-00020044.
XX
XX 10-SEP-2003; 2003US-0502163P.
XX
XX (WAKN) WARNER LAMBERT CO LLC.
XX (ABGE-) ABGENIX INC.
XX
XX Bedian V, Devalaraja MN, Low JE, Mobley JL, Kellermann S;
XX Poltz I, Haak-Frendescho M;
XX
XX MPI; 2005-216576/23.
XX
XX Novel humanized, chimeric or human monoclonal antibody e.g. 9.14.4I or
XX 8.10.3F antibody that binds to and inhibits human macrophage colony
XX stimulating factor, useful for producing medicament for treating
XX rheumatoid arthritis.
XX
XX Disclosure; SEQ ID NO 109; 155pp; English.
XX
XX The invention relates to a humanized, chimeric or human monoclonal
XX antibody (I) or its antigen-binding portion that binds specifically to
XX and inhibits human macrophage colony stimulating factor (M-CSF). Also
XX described: (1) a polypeptide chosen from AEA41017, AEA41019, AEA41021,
XX AEA41023, AEA41025, AEA41027, AEA41028, AEA41029, AEA41030, AEA41031,
XX AEA41033, AEA41035, AEA41037, AEA41039, AEA41041, AEA41043, AEA41045,
XX AEA41047, AEA41049, AEA41051, AEA41053, AEA41054, AEA41055, AEA41056,
XX AEA41057, AEA41058, AEA41059, AEA41061, AEA41062, AEA41063,
XX AEA41064, AEA41065, AEA41066, AEA41067 and AEA41068, without a signal
XX sequence; (2) a composition (II) comprising (I) and a carrier; (3) an
XX isolated cell line (III) for producing (I) or its antigen-binding portion
XX or heavy or light chain of (I) or antigen-binding portions; and (4)
XX producing (I). (I) is useful for producing a medicament for treating a

CC condition chosen from arthritis, psoriatic arthritis, rheumatoid
CC arthritis, gout, traumatic arthritis, rubella arthritis and acute
CC synovitis and other arthritic conditions, sepsis, septic shock, endotoxi-
CC shock, gram negative sepsis, toxic shock syndrome, Alzheimer's disease,
CC stroke, neurotrauma, asthma, adult respiratory distress syndrome,
CC cerebral malaria, tumor, and chronic pulmonary inflammatory disease,
CC preferably rheumatoid arthritis. The present sequence represents the
CC germline V kappa L5, J kappa 3 amino acid sequence, which is given in the
CC exemplification of the present invention.

SQ Sequence 108 AA:

Query Match 88.9%; Score 488; DB 9; Length 108;
Best Local Similarity 86.7%; Prod. No. 4, 5e-27;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps

Dd 1 ELTQSPSSVASVGVDRITTCRASGGSISWLMAYQHQPCKAPKLILYNSASSLSQSVPSRF 60
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 QMVGSPSSVASVGVDRITTCRASGGSISWLMAYQQKPKAPKRLIILYNSASSLSQSVPSRF 62

Dy 61 SGGSGGTDFSLTITSSLQFEDSATYYCOANSFPYTTCGCTKYELIKR 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 SGGSGGTDFLTITSSLQFEDFATYYCOANSPFTPTGPETKVDIRK 108

RESULT 15
ADP22216 ID ADP22216 standard; protein; 107 AA.
XX ADP22216;
DT 09-SEP-2004 (first entry)
DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:122.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFa antibody; anabolic; arteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW metastatic cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW reestenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.
XX
FN WO2004050683-A2.
PD 17-JUN-2004.
XX
FE 02-DEC-2003; 2003WO-US038281.
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klapamp S;
PI Haak-Frendricho M, Rathanaswami P, Pisot C, Liang ML, Lee R;
PI Marchalenchko K, Fegioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI: 2004-480601/45.
XX N-PsDB; ADP22215.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as Cancer, or immuno-mediated inflammatory diseases such as Rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 122, 213pp. English.

```

XX  The present invention describes a human monoclonal antibody (I1) that
CC specifically binds to tumour necrosis factor- $\alpha$  (TNF $\alpha$ ) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with
CC (1), and detecting the level of binding between the antibody and TNF $\alpha$  in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I1); and (4) inhibiting (M3) TNF $\alpha$  induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of
CC (I1). (I1) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipapillary, antineumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNF $\alpha$  antagonist. The antibody (I1) is useful in the preparation of
CC a medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases, such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$ 
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
XX  Sequence 107 AA:
XX
Query Match      88.7%; Score 487; DB 8; Length 107;
Best Local Similarity 89.5%; Pred. No. 5.35-27;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY  1  ELTOSPSSVSAVSDRYTITTRASOGISSWLAWYOHOGKAPKLLIYASSLSQGVPSRF 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  3  QMTSPSSVSAVSDRYTITTRASOGISSWLAWYQQRGKAPKLLIYASSLSQGVPSRF 62
QY  61  SGSGYGTDFSLTITSLQFEDSATYYCOQANSFYTFGGGTVEIK 105
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  63  SGSGSGTDFLTITSLQPEDPASYYCOQANSFYTFGGGTVEIK 107

```

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 9.95758 Seconds
(without alignments)
1024.243 Million cell updates/sec

Title: US-10-027-725A-12

Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPYTFGGTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	84.2	117	2	S46376 Ig kappa chain V-J
2	462	84.2	125	2	S40316 Ig kappa chain - h
3	459	83.6	125	2	S40333 Ig kappa chain V-J
4	455	82.9	125	2	S40339 Ig kappa chain V-J
5	454.5	82.8	124	2	S40336 Ig kappa chain V-J
6	454	82.7	130	2	S40368 Ig kappa chain - h
7	451	82.1	128	2	S46372 Ig light chain var
8	451	82.1	131	2	S40352 Ig kappa chain V-J
9	450	82.0	105	2	S36266 Ig lambda chain V
10	447	81.4	127	2	S40367 Ig kappa chain V-J
11	446	81.2	108	2	S19674 Ig kappa chain V r
12	446	81.2	132	2	S38646 Ig kappa chain V r
13	445	81.1	117	2	S46371 Ig kappa chain V-J
14	444	80.9	123	2	S40331 Ig kappa chain - h
15	444	80.9	132	2	S40334 Ig kappa chain - h
16	443	80.7	108	2	B49047 Ig kappa chain V r
17	441	80.3	108	2	S47182 Ig kappa chain - h
18	441	80.3	109	2	S31998 Ig kappa chain - h
19	441	80.3	124	2	S40318 Ig kappa chain V r
20	439.5	80.1	108	2	S30521 Ig kappa chain V r
21	439	80.0	129	2	S40369 Ig kappa chain - h
22	437	79.6	107	2	S36264 Ig lambda chain V
23	435.5	79.3	108	2	S34007 Ig kappa chain V r
24	435	79.2	108	1	K1HUBN Ig kappa chain V-I
25	434.5	79.1	107	2	S36275 Ig lambda chain V
26	434	79.1	108	1	K1HUMS Ig kappa chain V-I
27	434	79.1	108	2	S44122 Ig kappa chain V r
28	433	78.9	117	2	S21527 Ig kappa chain pre
29	432	78.7	108	2	S36283 Ig lambda chain V

30	431.5	78.6	107	2	S47183 Ig kappa chain - h
31	431	78.5	107	2	S36262 Ig lambda chain V
32	428	78.0	107	2	S36269 Ig lambda chain V
33	427	77.8	109	2	S31981 Ig kappa chain - h
34	426.5	77.7	107	1	K1HUBK Ig kappa chain V-I
35	426	77.6	108	2	S36277 Ig lambda chain V
36	426	77.6	109	2	S31979 Ig kappa chain - h
37	426	77.6	110	2	PN0535 Ig kappa chain V r
38	426	77.6	122	2	S40370 Ig kappa chain - h
39	426	77.6	141	2	A49134 Ig kappa chain V-I
40	424	77.2	107	2	I69017 anti-HIV envelope
41	424	77.2	108	1	K1HUME Ig kappa chain V-I
42	424	77.2	129	1	K1HUMK Ig kappa chain pre
43	423	77.0	108	1	K1HUGL Ig kappa chain V-I
44	423	77.0	108	1	K1HUBU Ig kappa chain V-I
45	423	77.0	126	2	S40335 Ig kappa chain V-J

ALIGNMENTS

RESULT 1

S46376 Ig kappa chain V-J region (73-14) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C/Accession: S46376; S38649

R/Benson, C.; Chaetagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination

A/Reference number: S46369; MUID:94313975; PMID:8039491

A/Accession: S46376

A/Molecule type: mRNA

A/Residues: 1-117 <BEN>

A/Cross-references: UNIPARC:UPI00001165A9; EMBL:Z27177; NID:9415969; PIDN:CAA81701.1; PIR

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/25-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 84.2%; Score 462; DB 2; Length 117;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYOHQGRAPKLLIYASASSLQGVPSRF 60

Db 12 QMTQSPSSVSASVGDRTVITCRASQDISWLAHYQKPKLLIYASASSLQGVPSRF 71

Qy 61 SGSGYGTDFSLITISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106

Db 72 SGSGSGTDFLTITISLQPEDFATYCCQANSFPYTFGGTKVEIKR 117

RESULT 2

S40316 Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40316

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40316

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-125 <KLE>

A/Cross-references: UNIPARC:UPI0000176CAD; EMBL:X72426

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/31-105/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 84.2%; Score 462; DB 2; Length 125;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Matches	91;	Conservative	5;	Mismatches	10;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	-----	--------	----	------	----

[illegible]

RESULT 3

Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40332; MUID:94080891; PMID:8258341
A:Accession: S40333
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KIE>
A:Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:9441354; PIDN:CAA51111.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin homology <IM>
C:34-108/Domain: immunoglobulin homology <IM>

Query Match	83.6%	Score 459;	DB 2;	Length 125;
Best Local Similarity	82.9%	Pred. No. 4.3e-32;		
Matches 87; Conservative	11;	Mismatches 7;	Indels 0;	Gaps 0

```

Qy      1 ELTSPSSVSAVSDRPTLTTCRASQGISWMLAWQHQPGLATLLYSASLOSQVPSNF 60
      :::::
Db      21 QMTSPSTLSAVGDRPTLTTCRASQGISWMLAWQKQKGAFLLLIYKASSLSQVPSNF 80
      :::::

Qy      61 SSGSGYGDFTSLTISLQPEDSATYYCOANSPYTFECQGTKEIK 105
      :::::
Db      81 SSSSSGTEFTLTISLQPDFAIYYCOANSPYTFECQGTKEIK 125
      :::::

```

RESULT 4

Ig kappa chain V-J region - human
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1994 #sequence __revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S40349
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40332; MUID:94080891; PMID:8258341
 A:Accession: S40349
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-125 <KL3>
 A:Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:9441386; PIDD:CAAS1127.1; P
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:33-107/Domain: immunoglobulin homology <IM>

Query Match	82.9%	Score 455	DB 2	Length 125
Best Local Similarity	84.9%	Pred. NO. 9.3e-32		
Matches 90; Conservative	7	Mismatches 9	Indels 0	Gaps 0

QY I ELTQSPSSVSVSVDGRLVTITCRASQGISSMLAWQHQPGRAPKLLIYSKSSSLDSGVPSRF 60
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Dd 20 QLTQSPPSSLSSVGRLVTITCRASQGISSALAAWQQNPGRAPKLLIYDASSLESSEVSRRF 79
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

QY 61 SGGSGYDTFSLTTISLPEDSATYYCOAANSPYTFGGGTQKVEIKR 106
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Dd 80 SGGSGGYDTFTLTISLPEDENATYYCOAFNTPLTFGGGTQKVEIKR 125
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

RESULT 5

Ig kappa chain V-J region - human
 C|Species: Homo sapiens (man)
 C|Date: 19-May-1994 #sequence _revision 26-May-1995 #text_change 21-Jan-2000
 C|Accession: S40336
 R|Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A|Title: Expressed human immunoglobulin cni genes and their hypermutation.
 A|Reference number: S40332; MUID:94080891; PMID:8258341
 A|Accession: S40336
 A|Status: preliminary; translation not shown
 A|Molecule type: mRNA
 A|Residues: 1-124 <KLE>
 A|Cross-references: UNIPARC:UPI0000116156; EMBL:X72446; NID:G441360; PIDN:CAA51114.1; PIR
 C|Superfamily: immunoglobulin V region; immunoglobulin homology
 C|Keywords: heterotetramer; immunoglobulin
 F|31-105/Domain: immunoglobulin homology <IMM>

Query Match	82.8%	Score 454.5	DB 2	Length 124
Best Local Similarity	84.1%	Pred. No. 1e-31		
Matches 90; Conservative 10; Mismatches				Indels 1; Gaps 1;

[illegible]

RESULT

Ig kappa chain human
 C|Species: Homo sapiens (man)
 C|Date: 06-Mar-1994 #sequence _revision 26-May-1995 #text_change 21-Jan-2000
 C|Accession: S40368
 R|Klein, R., Jaenichen, R., Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A|Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A|Reference number: S40312; WUID:94080891; PMID:8258341
 A|Accession: S40368
 A|Status: preliminary; translation not shown
 A|Molecule type: mRNA
 A|Residues: 1-130 <KLE>
 A|Cross-references: UNIPARC:UP10000116176; EMBL:X72478; NID:9441424; PIDN:CA451146.1; PIR
 C|Superfamily: immunoglobulin V region; immunoglobulin homology
 C|Keywords: heterodimer; immunoglobulin
 F|33-107/Domain: immunoglobulin homology <IMM>

Query Match	82.7%;	Score 454;	DB 2;	Length 130;
Best Local Similarity	83.0%;	Pred. No. 1.2e-31;		
Matches 88; Conservative	7;	Mismatches 11;	Indels 0;	Gaps 0;

[illegible]

RESULT

s50312
 IG light chain variable region (VJ) - human
 C:Species: Homo sapiens (man)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S46372
 R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene re

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46372

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <BEN>

A:Cross-references: UNIPARC:UPI0000176CA4; EMBL:227173

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 128;

Best Local Similarity 83.8%; Pred. No. 2.1e-31;

Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 61

DB 24 LTQSPSSLASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASLTQGVPSRF 83

QY 62 GSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106

DB 84 GSGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 8

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40352

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <KLE>

A:Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:9441392; PIDN:CAA51130.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 131;

Best Local Similarity 83.0%; Pred. No. 2.1e-31;

Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60

DB 23 QMTQSPSSLASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASLTQGVPSRF 82

QY 61 GSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106

DB 83 GSGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 9

Ig lambda chain V region (clone alpha-TNF-E1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C:Accession: S36266

R:Griffiths, A.D.; Malgouyret, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A>Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36266; MUID:93178448; PMID:7679990

A:Accession: S36266

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-105 <GRI>

A:Cross-references: UNIPARC:UPI0000118DF2; EMBL:Z18840; NID:933423; PIDN:CAA79292.1; PID

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 450; DB 2; Length 105;

Best Local Similarity 85.3%; Pred. No. 2.1e-31;

Matches 87; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 LTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 61

DB 4 LTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASLTQGVPSRF 63

QY 62 GSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 103

DB 64 GSGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 105

RESULT 10

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40367

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 447; DB 2; Length 127;

Best Local Similarity 82.1%; Pred. No. 4.5e-31;

Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60

DB 20 QMTQSPSSLASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASLTQGVPSRF 79

QY 61 GSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 106

DB 80 GSGSGTDFSLTISLQPEDSATYCCQANSFPYTFGGTKVEIKR 125

RESULT 11

Ig kappa chain V region (clone alpha-TEL9) - human

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19674

R:Marke, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.

Mol. Biol. 222, 581-597, 1991

A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19674

A:Molecule type: mRNA

A:Residues: 1-108 <MAR>

A:Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:937860; PIDN:CAA3823.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.2%; Score 446; DB 2; Length 108;

Best Local Similarity 82.9%; Pred. No. 4.7e-31;

Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 61

DB 4 LTQSPSSLASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYAASLTQGVPSRF 63

Qy 62 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106
 Db 64 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 108

RESULT 12

S38646
 Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S38646

R/Bensimon, C.; Chastagner, P.; Zouali, M.

Submitted to the EMBL Data Library, November 1993

A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.

A/Reference number: S38643

A/Accession: S38646

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <BEN>

A/Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/40-114/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 132;
 Best Local Similarity 82.9%; Pred. No. 5.6e-31;
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGDVVTITCRASQGISLWAWYQHOGKAPKLLIYSASSLSQGVPSRF 61
 Db 28 IAGSPSSLSASVGDVVTITCRASQGISLWAWYQOKKPKAPKLLIYAASTLSQGVPSRF 87

Qy 62 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106
 Db 88 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 132

RESULT 13

S46371
 Ig kappa chain V-J region (724-3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C/Accession: S46371; S38645

R/Bensimon, C.; Chastagner, P.; Zouali, M.

EMBL J. 13, 2951-2962, 1994

A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene ree

A/Reference number: S46369; MUID:94313975; PMID:8039491

A/Accession: S46371

A/Molecule type: mRNA

A/Residues: 1-117 <BEN>

A/Cross-references: UNIPARC:UPI00001165A4; EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/23-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 445; DB 2; Length 117;
 Best Local Similarity 78.7%; Pred. No. 6.1e-31;
 Matches 85; Conservative 14; Mismatches 7; Indels 2; Gaps 1;

Qy 1 ELTQSPSSVSASVGDVVTITCRASQGISLWAWYQHOGKAPKLLIYSASSLSQGVPSRF 60
 Db 10 QMTQSPSTLSASVGDVVTITCRASRSISTWLAWYQOKKPKAPKLLIYKASTLSQGVPSRF 69

Qy 61 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106
 Db 70 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 117

RESULT 14

S40331

Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40331
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40331

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <KLE>

A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 123;
 Best Local Similarity 83.8%; Pred. No. 7.8e-31;
 Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITCRASQGISLWAWYQHOGKAPKLLIYSASSLSQGVPSRF 60
 Db 19 QMTQSPSTLSASVGDVVTITCRASQGISLWAWYQOKKPKAPKLLIYAASTLSQGVPSRF 78

Qy 61 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 105
 Db 79 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 123

RESULT 15

S40334
 Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40334

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40334

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-132 <KLE>

A/Cross-references: UNIPARC:UPI0000176CA9; EMBL:X72444

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 132;
 Best Local Similarity 80.2%; Pred. No. 8.3e-31;
 Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITCRASQGISLWAWYQHOGKAPKLLIYSASSLSQGVPSRF 60
 Db 24 QLTQSPSTLSASVGDVVTITCRASQGISLWAWYQOKKPKAPKLLIYVASTLSQGVPSRF 83

Qy 61 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106
 Db 84 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 129

Search completed: August 30, 2006, 00:42:54
 Job time: 9.95758 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 57.8182 Seconds
(without alignments)

1695.862 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTGSPSSVASVGDVIT.....QANSPFYFGGKTVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	88.0	236	2	O6GMX8 HUMAN
2	444	80.9	236	2	O6GMW1 HUMAN
3	443	80.7	236	2	O6PIH7 HUMAN
4	437	79.6	108	2	O9UL70 HUMAN
5	437	79.6	108	2	O9UL77 HUMAN
6	435	79.2	108	1	KV1V HUMAN
7	434	79.1	108	1	KV1S HUMAN
8	434	79.1	108	2	O9UL79 HUMAN
9	429	78.1	236	2	O502W4 HUMAN
10	429	78.1	236	2	O6GMX9 HUMAN
11	427	77.8	244	2	O65ZC8 HUMAN
12	426.5	77.7	107	1	KV1D HUMAN
13	426.5	77.6	107	2	O96S89 HUMAN
14	426	77.6	234	2	O7Z473 HUMAN
15	425	77.4	236	2	O7Z3Y4 HUMAN
16	424	77.2	108	1	KV1R HUMAN
17	424	77.2	129	1	KV1W HUMAN
18	424	77.2	236	2	O6PIH5 HUMAN
19	423	77.0	108	1	KV1G HUMAN
20	423	77.0	108	1	KV1H HUMAN
21	423	77.0	240	2	O65ZC9 HUMAN
22	419	76.3	108	1	KV1P HUMAN
23	419	76.3	108	1	KV1L HUMAN
24	419	76.3	189	2	O56917 HUMAN
25	416	75.8	108	1	KV1O HUMAN
26	416	75.8	236	2	O6GMX0 HUMAN
27	416	75.8	236	2	O6PIH4 HUMAN
28	413	75.2	108	1	KV1B HUMAN
29	411.5	75.0	107	2	O9UL81 HUMAN
30	410	74.7	108	1	KV1M HUMAN
31	408	74.3	108	1	KV1E HUMAN

32	406	74.0	108	1	KV1A HUMAN	P01593 homo sapien
33	405	73.8	108	1	KV1P HUMAN	P01608 homo sapien
34	403	73.4	234	2	O5E6F6 HUMAN	O5E6F6 homo sapien
35	402	73.2	117	1	KV1I HUMAN	P01601 homo sapien
36	401	73.0	108	1	KV1N HUMAN	P01606 homo sapien
37	401	73.0	108	1	KV1J HUMAN	P80362 homo sapien
38	394	71.8	117	1	KV1J HUMAN	P01602 homo sapien
39	393	71.6	108	1	KV1C HUMAN	P01595 homo sapien
40	391	71.2	108	1	KV1K HUMAN	P01603 homo sapien
41	385	70.1	108	1	KV1Q HUMAN	P01609 homo sapien
42	385	70.1	129	1	KV1X HUMAN	P04432 homo sapien
43	383	69.8	108	1	KV5S_MOUSE	P01652 mus musculu
44	382	69.6	108	2	O9UL83 HUMAN	Q9UL83 homo sapien
45	380	69.2	108	1	KV5Q_MOUSE	P01650 mus musculu

ALIGNMENTS

RESULT 1
O6GMX8 HUMAN
ID O6GMX8 PRELIMINARY; PRT; 236 AA.
AC O6GMX8;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGC protein.
GN Name=IGC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
XP [1]
RA NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunter P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,
RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC EMBL; BC073764; AA073764.1; -; mRNA.
DR SNR; O6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.

```

DR InterPro; IPR003596; IG V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SMO0409; IG; 1.
DR SMART; SMO0407; IGCL; 1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
DR SEQUENCE 236 AA; 25707 MW; 4FC8E1AB659EF9C CRC64;

Query Match      88.0%; Score 483; DB 2; Length 236;
Best Local Similarity 87.7%; Fred. No. 5.3e-42;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTSPSSVSASVGDRTVTITRASGIGISMTLAWYOHCPKAPKLITYSASSLSGSVPSERF 60
   :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 25 QMTSPSSVSASVGDRTVTITTRASGIGISMTLAWYQHCKGKAPKLITYAASSLSGSVPSERF 84
   :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 SGSGYGTDPSLTITSLSPEDSATYYCCQAANSEPFYFGCGTKVEIKR 106
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 85 SGSGYGTDPSLTITSLSPEDPATYYCCQAHSPPFPFPGGTIVDIR 130
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2
OG6MM1_HUMAN
ID OG6MM1_HUMAN PRELIMINARY; PRT; 236 AA.
AC OG6MM1;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGKC protein.
GN Name=IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_Taxid=9606;
[1]
NP NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Scheaffer C.F., Bat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heseltine P.,
RA Diatchenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
FA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.T., Skalska U., Smalins D.E.,
RA Schercher A., Schön J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen.
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/genbank/DBD databases.
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CC EMBL; BC073791; AAH73791.1; -; mRNA.
SMR OG6MM1_24-236.
DR Ensembl; ENSG00000165245; Homo sapiens.
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CC InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003068; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SMO0409; Ig; 1.
DR SMART; SMO0407; IGc1; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
DR PROSITE; PSM0290; IG_MHC; UNKNOWN; 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087AFAC437 CRC64;

Query Match 80.9%; Score 444; DB 2; Length 236;
Best Local Similarity 82.1%; Pred. No. 6, 2e-38;
Matches 87; Conservative 10; Mismatches 9; Indels 0; Gaps

DY 1 ELTQSPBSVASVSGDRTVTTCRASOGISMTLAMYQHOPKAPLTLLYSASSLOSQPNSF
DY QMTPSSPSLSAVSAGDRITTCRASGGSIDSLGWQQPGAPALTLLIYAASSLOSQVSRRF
Db 25
OY 61 SGSGYGTFDSLTISSIQFDSEATYYCQAANSFPPTFGOSTKEIKR 106
Db 85 SGSGSGSTDFTLTISSLQPEDPFTYYCLQDPYNWWTGGQGKEIKR 130

RESULT 3
OSPIH7 HUMAN PRELIMINARY; PRt; 236 AA.

ID OSPIH7 AC OGPRI7 DT 05-JUL-2004 integrated into UniProtKB/TREMBL.
DT 05-JUN-2004 sequence version 1.
DT 07-FEB-2006 entry version 17.
DE IKKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mamalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_taxonomy:9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Lung;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bluetow K.H., Schafer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadlton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toobyhyki S., Carninci P., Mullany S.J.,
RA Raha S.S., Loggiano N.A., Peters G.U., Abramson R.D., Mulvaney S.J.,
RA Bosak S.A., McGowan P.O., McKernan R.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Huliyil S.W.,
RA Villalón D.K., Munzky D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Botterfield Y.S.N., Krzywinska M.I., Skalska U., Smalls D.E.,
RA Genereich A., Schein J.E., Jones S.U.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
LN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
NP NUCLEOTIDE SEQUENCE.
RC Tissue=Lung;
RG NIH MGC Project;
CC Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

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CC EMBL; BC034141; AAB34141.1; -, mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 80.7%; Score 443; DB 2; Length 236;
Best Local Similarity 83.0%; Pred. No. 7.9e-38;
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVGVDRVTITCRASQGISWLAHYQHQPGRAPKLLIYSASLSQGVPSRF 60
DB 25 QLTQSPSSLSASVGDRTITCRASQGISWLAHYQKPKRPNLLIYAASLTQSGVPSRF 84
QY 61 SSGSGTDPSTLTSSLSQFEDSATIYCOQANSFPTTGGQTKVEIKR 106
DB 85 SSGSGTDPSTLTSSLSQFEDSATIYCOQANSFPTTGGQTKVEIKR 130

RESULT 4
Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92078975; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idio-type.";
RL J. Exp. Med. 174:1639-1652(1991).

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CC EMBL; AF035044; AAD56280.1; -, mRNA.
DR PIR; P01607; 1BWM.
DR HSSP; P01607; 1BWM.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
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DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1 108
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.4e-37;
Matches 85; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVGVDRVTITCRASQGISWLAHYQHQPGRAPKLLIYSASLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTITCRASQGISWLAHYQKPKRPNLLIYAASLTQSGVPSRF 62
QY 61 SSGSGTDPSTLTSSLSQFEDSATIYCOQANSFPTTGGQTKVEIKR 106
DB 63 SSGSGTDPSTLTSSLSQFEDSATIYCOQANSFPTTGGQTKVEIKR 108

RESULT 5
Q9UL77 HUMAN PRELIMINARY; PRT; 108 AA.
ID Q9UL77;
AC Q9UL77;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92387224; PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Iuzza L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).

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CC EMBL; AF035037; AAD56273.1; -, mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWM.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
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DR SMART: SM00406; IGV: 1.
DR PROSITE; PSS0835; IG LIKE: 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16P3 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 81.1%; Pred. No. 1.4e-37;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHQPGRKPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQGISSTYLNWYQGRKPKLLIYAASSLSQGVPSRF 62
Qy 61 SGSGYGTDFSLTITSSLPEDSATIYYCOQANSFPYFGQGTKEIKR 106
Db 63 TSGSGGTDFLTITSSLPEDFATYYCOQSYSTSWTFEGGTKEIKR 108

RESULT 6
KV1V_HUMAN STANDARD; PRT; 108 AA.
ID KV1V_HUMAN
AC P04430;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=66174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwyler F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC -----
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CC PIR: A01878; KIHUMS.
DR HSSP; P04430; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE: 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1
FT REGION 1 23 Ig kappa chain V-I region BAN.
FT REGION 24 34 /FTID=PRO_0000059756.
FT REGION 35 49 Framework-1.
FT REGION 50 56 Complementarity-determining-1.
FT REGION 57 88 Framework-2.
FT REGION 89 97 Complementarity-determining-2.
FT REGION 98 97 Framework-3.
FT REGION 99 107 Complementarity-determining-3.
FT DISULFID 23 107 Framework-4.
FT NON_TER 23 88 By similarity.
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 79.2%; Score 435; DB 1; Length 108;

Best Local Similarity 78.3%; Pred. No. 2.3e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHQPGRKPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQGISSTYLNWYQGRKPKLLIYAASSLSQGVPSRF 62
Qy 61 SGSGYGTDFSLTITSSLPEDSATIYYCOQANSFPYFGQGTKEIKR 106
Db 63 TSGSGGTDFLTITSSLPEDFATYYCOQSYSTSWTFEGGTKEIKR 108

RESULT 7
KV1S_HUMAN STANDARD; PRT; 108 AA.
ID KV1S_HUMAN
AC P01611;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 40.
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by high-pressure liquid chromatography. The primary structure of a monoclinal L-chain of k-type, subgroup I (Bence-Jones protein Wes).";
RL Hoppe-Seyler's Z. Physik. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC PIR: A01877; KIHUMS.
DR HSSP; P01611; 2-108.
DR SMR; P01611; 2-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE: 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1
FT REGION 1 23 Ig kappa chain V-I region Wes.
FT REGION 24 34 Framework-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-1.
FT REGION 57 88 Framework-2.
FT REGION 89 97 Complementarity-determining-2.
FT REGION 98 97 Framework-3.
FT REGION 99 107 Complementarity-determining-3.
FT DISULFID 23 107 Framework-4.
FT NON_TER 23 88 By similarity.
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 79.1%; Score 434; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 2.9e-37;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Db 3 QMSPSSVSASVGDRTVITCRASQDISHWLAWYQQSAGKAPKLLIYSASLSLGVSRF 62
 QY 61 GSGGYGDFSLTSSLOFEDSATYCCQANSFPPTPGGTKEIKR 106
 DB 63 GSGSGTEFTLTISLOPEDFATYFCQAHASVPLTFGGTIVDIKR 108

RESULT 8

Q9UL79_HUMAN PRELIMINARY; PRT; 108 AA.
 ID Q9UL79_HUMAN
 AC Q9UL79;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 NUCLEOTIDE SEQUENCE.
 RP MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 [2]
 NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92289816; PubMed=1601042;
 RA Huber C., Klobbeck H.G., Zachau H.G.;
 RT "ongoing V kappa-J kappa recombination after formation of a productive
 V kappa-J kappa coding joint";
 RL Eur. J. Immunol. 22:1561-1565(1992).
 [3]
 NUCLEOTIDE SEQUENCE.
 RP MEDLINE=93170387; PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation";
 RL Eur. J. Immunol. 23:391-397(1993).
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 CC -----
 CC EMBL: AF035035; AAD56271.1; -; mRNA.
 CC PIR: S23638; S23638.
 CC PIR: S30521; S30521.
 CC PIR: S34090; S34090.
 CC HSSP: P01607; 1BMW.
 CC SWR: Q9UL79; 1-10W.
 CC Linkhub: Q9UL79; -;
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003596; Ig_v.
 CC InterPro: IPR013106; V-set.
 CC SMART: SM00409; IG; 1.
 CC SMART: SM00406; IG; 1.
 CC PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin domain.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBA4 CRC64;

Query Match 79.1%; Score 434; DB 2; Length 108;

Best Local Similarity 81.0%; Pred. No. 2.3e-37;

Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

2 LTSPSSVSASVGDRTVITCRASQDISHWLAWYQQSAGKAPKLLIYSASLSLGVSRF 61

Db 4 MTPSPILLSASTGDRVTISCRMSQGISSYLAWYQQRKAPKPELLIYASTLQSGVSRF 63
 QY 62 GSGGYGDFSLTSSLOFEDSATYCCQANSFPPTPGGTKEIKR 106
 DB 64 GSGSGTEFTLTISLOPEDFATYFCQAHASVPLTFGGTIVDIKR 108

RESULT 9

O502M4_HUMAN PRELIMINARY; PRT; 236 AA.
 ID O502M4_HUMAN
 AC O502M4;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-JUN-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 NUCLEOTIDE SEQUENCE.
 RP TISSUE=gladular pool- thyroid;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 NUCLEOTIDE SEQUENCE.
 RP TISSUE=gladular pool- thyroid;
 RC NIH MGC Project;
 RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: BC095489; AAH95489.1; -; mRNA.
 CC Ensembl: ENSG00000163245; Homo sapiens.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003597; Ig_c1.
 CC InterPro: IPR003006; IG_v.
 CC InterPro: IPR003596; IG_v.
 CC Pfam: PF07654; C1-set; 1.
 CC SMART: SM00409; IG; 1.
 CC SMART: SM00407; IGc1; 1.
 CC SMART: SM00406; IG; 1.
 CC PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756A9 CRC64;

Query Match 78.1%; Score 429; DB 2; Length 236;

Best Local Similarity 79.2%; Pred. No. 2.3e-36;

Matches 84; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Oy ELTOSPESSVSAVSDRATLTTCRASQGISSMLAWOHOPGAKPLTLVSASSLQSGVPSRF 6
 Db 25 QMTSPSSLSVSDRATLTTCRASQGIIRNDLGMVQQPEGAPRRLTFASSLSQGVPSRF 84
 Oy 61 SSGSGYGTDFSLTTLISLQFEDSATATYCCOANSFPYTFGQGTKEIKR 106
 Db 85 SSSSGTREFTLTINSLQPEDPATYTCGLQYNSYPTFGQGTKEIKR 130
 RESULT 10
 O6GMX9 HUMAN
 ID O6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.
 AC O6GMX9?
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human) .
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE. -
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepchenko M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Bottingfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: BC073763; AAH73763.1; -, mRNA.
 DR SMR: O6GMX9; 23-236.
 DR Ensemble: ENSG00000163245; Homo sapiens.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-CL.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR013106; V-set.
 DR Pfam: PF07654; CL-set; 1.
 DR SMART: SM00409; IGV.1.
 DR SMART: SM00407; IGC1.1.
 DR SMART: SM00406; IGV.1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKOWN 1.
 SQ SEQUENCE 236 AA; 25924 MW; FBE2093DC560CFF7 CRC64;

Query Match	78.1%; Score 429; DB 2; Length 236;
Best Local Similarity	78.3%; Pred. No. 2.3e-36;
Matches 83; Conservative	9; Mismatches 14; Indels 0; Gaps 0;
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Dd	25 QMTQSPPSLASVGHRYITICRASNYSRWLAHYQORPEKAPKLIYATSSLHSGVPSRF 84 ::
Oy	61 SGGSGVDPLSLTISLQFEDSATYYCOANSEPYTFGGGTVEIKR 106 ::
Dd	85 SGGSGVDPLSLTISLQFEDPATYYCOANTYPITFGGCTVEIKR 130 ::
RESULT 11	
O65ZC8 HUMAN	PRELIMINARY; PRT; 244 AA.
AC O65ZC8_HUMAN	PRELIMINARY; PRT; 244 AA.
DT 11-OCT-2004,	integrated into UniProtKB/TREMBL.
DT 11-OCT-2004,	sequence version 1.
DT 07-FEB-2006,	entry version 9.
DE Single-chain Fv (Fragment).	
GN Name=scFv;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;	
RA Kontermann R.B., Wing M.G., Winter G.;	"Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).	
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DR DR EMBL, Y13057; CAA73500.1; -; mRNA.	
DR InterPro; IPR003599; IG_	
DR InterPro; IPR007110; IG-like.	
DR InterPro; IPR003596; IG_V.	
DR InterPro; IPR013106; V-set.	
DR SMART; SM00409; IG; 2.	
DR SMART; SM00406; IGV; 2.	
DR PROSITE; PS50835; IG-LIKE; 2.	
KW Immunoglobulin domain.	
FT NON TER	1
SQ SEQUENCE	244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
Query Match	77.8%; Score 427; DB 2; Length 244;
Best Local Similarity	75.5%; Pred. No. 3.9e-36;
Matches 80; Conservative	13; Mismatches 13; Indels 0; Gaps 0;
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Dd	139 QMTQSPPSLASVGHRYITICRASNGIHWLAHYQOKRGKAPKLIYASSLSAGAPSRF 198 ::
Oy	61 SGGSGVDPLSLTISLQFEDSATYYCOANSEPYTFGGGTVEIKR 106 ::
Dd	199 SGGSGVDPLSLTISLQFEDPATYYCOQSYSNYPITFGGCTVEIKR 244 ::
RESULT 12	
KVID_HUMAN	STANDARD; PRT; 107 AA.
AC P01596;	
DT 21-JUL-1986,	integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986,	sequence version 1.
DT 07-MAR-2006,	entry version 38.
DE Ig kappa chain V-I region CAR.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=75075135; PubMed=4216454;
 RA "Milestone C.P., Deverson E.V.;
 RT "Primary structure of kappa light chain from a human myeloma
 RT protein";
 RL Eur. J. Biochem. 49:377-391(1974).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
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 CC -----
 DR PIR; A01864; KIHUAR.
 DR HSSP; P80362; 1MTL.
 DR SMR; P01596; 1-107.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig V.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KM Immunoglobulin V region.
 FT CHAIN 1 >107
 FT CARBOHYD 28
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11704 MW; E1BF0DF9844C3346 CRC64;
 Query Match 77.7%; Score 426.5; DB 1; Length 107;
 Best Local Similarity 76.4%; Pred. No. 1.7e-36;
 Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;
 QY 1 ELTQSSSVASVGVDRVTTCRASQGISWLMWYOHQPKAPKLLTYSSLSQSGVPSRF 60
 DB 3 QMTQSSSTLSASVGRVATTCRASQNISWLMWYQOKPKAPKLLTYSSLSQSGVPSRF 62
 QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 106
 DB 63 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 107
 RESULT 13
 Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.
 AC Q96SA9;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 18.
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 RT antibody V region genes";

RL J. Immunol. 161:2020-2031(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92387224; PubMed=1516616;
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
 RT "Human monoclonal stritacinal autoantibodies isolated from thymic B
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene
 RT segments associated with the autoimmune repertoire";
 RL Eur. J. Immunol. 22:2231-2236(1992).
 CC [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93170387; PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation";
 RL Eur. J. Immunol. 23:391-397(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
 RA Diamond B.;
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idiotype";
 RL J. Exp. Med. 174:1639-1652(1991).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91243737; PubMed=1903706;
 RA Blaison G., Kuntz J.L., Pasquall J.L.;
 RT "Molecular analysis of V kappa III variable regions of polyclonal
 RT rheumatoid factors during rheumatoid arthritis";
 RL Eur. J. Immunol. 21:1221-1227(1991).
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 CC -----
 DR EMBL; U96396; AAB68785.1; -; mRNA.
 DR PIR; B49047; B49047.
 DR PIR; PH0867; PH0867.
 DR PIR; S16840; S16840.
 DR PIR; S31977; S31977.
 DR PIR; S34083; S34083.
 DR PIR; S34086; S34086.
 DR HSSP; P01607; 1BMW.
 DR SMR; Q96SA9; 1-107.
 DR Ensemble; ENSG00000163245; Homo sapiens.
 DR LinkHub; Q96SA9; -;
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig V.
 DR InterPro; IPR013106; V-set.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin domain.
 FT NON TER 1
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;
 Query Match 77.7%; Score 426.5; DB 2; Length 107;
 Best Local Similarity 82.1%; Pred. No. 1.7e-36;
 Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;
 QY 1 ELTQSSSVASVGVDRVTTCRASQGISWLMWYOHQPKAPKLLTYSSLSQSGVPSRF 60
 DB 3 QMTQSSSTLSASVGRVATTCRASQISWLMWYQOKPKAPKLLTYSSLSQSGVPSRF 62
 QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 106
 DB 63 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 107
 RESULT 14

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 14.4545 Seconds
(without alignments)
641.891 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGRVITTT.....OQANSPPYFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/prodata/2/1aa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/prodata/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/prodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	94.4	233	2	US-08-812-586-45 Sequence 45, Appl
2	518	94.4	233	2	US-09-535-832A-42 Sequence 42, Appl
3	475	86.5	236	2	US-09-859-053-30 Sequence 30, Appl
4	466	84.9	108	2	US-09-970-262A-8 Sequence 8, Appl
5	466	84.9	109	1	US-07-934-373C-3 Sequence 3, Appl
6	466	84.9	109	2	US-08-437-642B-3 Sequence 3, Appl
7	466	84.9	109	2	US-08-146-206C-3 Sequence 3, Appl
8	466	84.9	109	2	US-09-705-686-3 Sequence 3, Appl
9	466	84.9	109	2	US-09-705-392A-3 Sequence 3, Appl
10	466	84.9	109	2	US-09-705-398-3 Sequence 3, Appl
11	466	84.9	109	5	PCT-US93-07832-3 Sequence 3, Appl
12	464.5	84.6	109	2	US-09-798-058-4 Sequence 4, Appl
13	463	84.3	107	2	US-09-240-274-40 Sequence 40, Appl
14	463	84.3	107	1	US-09-848-798-40 Sequence 40, Appl
15	460	83.8	107	1	US-08-276-852-104 Sequence 104, App
16	460	83.8	107	1	US-08-899-575-104 Sequence 104, App
17	460	83.8	107	2	US-08-899-575-104 Sequence 104, App
18	460	83.8	107	2	US-09-644-668A-13 Sequence 13, Appl
19	460	83.8	107	5	PCT-US95-08743-104 Sequence 104, App
20	460	83.8	108	2	US-08-974-899-3 Sequence 3, Appl
21	460	83.8	108	2	US-09-795-798-3 Sequence 3, Appl
22	460	83.8	108	2	US-08-908-469-12 Sequence 12, Appl
23	459	83.6	128	1	US-08-259-372A-14 Sequence 14, Appl
24	459	83.6	128	1	US-08-468-671-14 Sequence 14, Appl
25	457	83.2	107	1	US-08-276-852-84 Sequence 84, Appl
26	457	83.2	107	1	US-08-899-575-84 Sequence 84, Appl

27	457	83.2	107	1	US-08-899-575-84 Sequence 84, Appl
28	457	83.2	107	2	US-09-240-274-175 Sequence 175, App
29	457	83.2	107	2	US-09-240-274-176 Sequence 176, App
30	457	83.2	107	2	US-09-848-798-175 Sequence 175, App
31	457	83.2	107	2	US-09-848-798-176 Sequence 176, App
32	457	83.2	107	5	PCT-US95-08743-104 Sequence 104, App
33	456	83.1	107	2	US-09-240-274-156 Sequence 156, App
34	456	83.1	107	2	US-09-848-798-156 Sequence 156, App
35	456	83.1	109	2	US-09-157-370-3 Sequence 3, Appl
36	455	82.9	107	1	US-07-934-373C-18 Sequence 18, Appl
37	455	82.9	107	2	US-08-437-642B-18 Sequence 18, Appl
38	455	82.9	107	2	US-08-146-206C-18 Sequence 18, Appl
39	455	82.9	107	2	US-09-648-067A-14 Sequence 14, Appl
40	455	82.9	107	2	US-09-705-686-18 Sequence 18, Appl
41	455	82.9	107	2	US-09-705-392A-18 Sequence 18, Appl
42	455	82.9	107	2	US-09-705-398-18 Sequence 18, Appl
43	455	82.9	107	2	US-09-602-812A-5 Sequence 5, Appl
44	455	82.9	107	5	PCT-US93-07832-18 Sequence 18, Appl
45	454	82.7	109	2	US-09-025-769B-28 Sequence 28, Appl

ALIGNMENTS

```
RESULT 1
US-08-812-586-45
; Sequence 45, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ. ID NO.: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-586-45
;
; Query Match 94.4%; Score 518; DB 2; Length 233;
; Best local Similarity 96.2%; Pred. No. 4.3e-41;
; Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 ELTQSPSSVSASVGRVITTTTCRASQGISGLAWYQHQPGRKRLTLTSSLSQGVPSRF 60
DB 23 ELTQSPSSVSASVGRVITTTTCRASQGISGLAWYQHPGRKRLTLTSSLSQGVPSRF 82

Qy 61 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 106
Db 83 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 128

RESULT 2
US-09-535-832A-42
; Sequence 42, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-A2
; CURRENT APPLICATION NUMBER: US/09/535, 832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-42

Query Match 94.4%; Score 518; DB 2; Length 233;
Best Local Similarity 96.2%; Pred. No. 4.3e-41;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYASASSLQSGVPSRF 60
Db 23 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYASASSLQSGVPSRF 82

Qy 61 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 106
Db 83 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 128

RESULT 3
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859, 053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match 86.5%; Score 475; DB 2; Length 236;
Best Local Similarity 88.7%; Pred. No. 4.6e-37;
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYASASSLQSGVPSRF 60
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISRLLAHYQHPGKAPKLLIYASSLQSGVPSRF 84

Qy 61 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 106
Db 85 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 130

RESULT 4
US-09-920-262A-8
; Sequence 8, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920, 262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-8

Query Match 84.9%; Score 466; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.4e-36;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYASASSLQSGVPSRF 60
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYASSLQSGVPSRF 62

Qy 61 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 106
Db 63 SGGSGTDFSLTITSSLOPEDSATYTCQOANSFPTFGGKTVEIKR 108

RESULT 5
US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Prestia
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934, 373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-3

Query Match 84.9%; Score 466; DB 1; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDVVTITTCRASQGISWLMAYOHQPKAPKLLIYASSLQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDVVTITTCRASQDVSSYLAWYQKPKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYTDPSLTITSSIQFEDSATYTCQANSPPYTFGGGTKEIKR 106
DB 63 SSGSGSTDFLTITSSIQPEDFATYTCQQYNSLPYTFGGGTKEIKR 108

RESULT 6
US-08-437-642B-3
Sequence 3, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-3

Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDVVTITTCRASQGISWLMAYOHQPKAPKLLIYASSLQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDVVTITTCRASQDVSSYLAWYQKPKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYTDPSLTITSSIQFEDSATYTCQANSPPYTFGGGTKEIKR 106
DB 63 SSGSGSTDFLTITSSIQPEDFATYTCQQYNSLPYTFGGGTKEIKR 108

RESULT 7
US-08-146-206C-3
Sequence 3, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-3

Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDVVTITTCRASQGISWLMAYOHQPKAPKLLIYASSLQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDVVTITTCRASQDVSSYLAWYQKPKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYTDPSLTITSSIQFEDSATYTCQANSPPYTFGGGTKEIKR 106
DB 63 SSGSGSTDFLTITSSIQPEDFATYTCQQYNSLPYTFGGGTKEIKR 108

RESULT 8
US-09-705-686-3
Sequence 3, Application US/09705686
Patent No. 663905
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3
Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVASVGDVVTITTCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGRVITTCRASQGVDSYLAHYQPKAPKLLIYASASSLSQGVPSRF 62
Qy 61 SSGSGVTDPSLTISLTQPEDSATYTCQANSPFYTTGGGTKEIKR 106
Db 63 SSGSGGTDFLTITISLTQPEDPATYTCQYNSLPYTTGGGTKEIKR 108
RESULT 9
US-09-705-392A-3
Sequence 3, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-392A-3

Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVASVGDVVTITTCRASQGISWLAHYQHQPCKAPKLLIYASASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGRVITTCRASQGVDSYLAHYQPKAPKLLIYASASSLSQGVPSRF 62
Qy 61 SSGSGVTDPSLTISLTQPEDSATYTCQANSPFYTTGGGTKEIKR 106
Db 63 SSGSGGTDFLTITISLTQPEDPATYTCQYNSLPYTTGGGTKEIKR 108
RESULT 10
US-09-705-398-3
Sequence 3, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-No. 6800738-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993


```

; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-3

Query Match      84.9%; Score 466; DB 5; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy
1 ELTQSPSSVASVGDRTVITTCRASQGISWLAWOHOPGAPKLLIYSASSLSQGVPSRF 60
Db
3 QMTQSPSSLASVGDRTVITTCRASQDVSVSLAWYQOKPKRAPKLLIYAASSLSQGVPSRF 62

Qy
61 SSGSGYGFDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db
63 SSGSGGDFLTLTISLQPEDFATYCCQYNSLPYTFGQGTKEIKR 108

RESULT 12
US-09-798-058-4
; Sequence 4, Application US/09798058
; Patent No. 6946546
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Vaughan, Alison Jane
; APPLICANT: Smith, Stephen
; APPLICANT: Main, Sarah Helen
; TITLE OF INVENTION: Human antibodies against eotaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-058-4

Query Match      84.6%; Score 464.5; DB 2; Length 109;
Best Local Similarity 86.0%; Pred. No. 2e-36;
Matches 92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy
1 ELTQSPSSVASVGDRTVITTCRASQGISWLAWOHOPGAPKLLIYSASSLSQGVPSRF 60
Db
3 QMTQSPSSVASVGDRTVITTCRASQDVSVSLAWYQOKPKRAPKLLIYAASSLSQGVPSRF 62

Qy
61 SSGSGYGFDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db
63 SSGSGGDFLTLTISLQPEDFATYCCQASSFPYTFGQGTKEIKR 109

RESULT 13
US-09-240-274-40
; Sequence 40, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rb(D)-BINDING PROMETINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-40

```

Query Match	84.3%;	Score 463;	DB 2;	Length 107;
Best Local Similarity	85.8%;	Pred. No. 2.7e-3e;		
Matches	91;	Conservative	7;	Mismatches 8;
			Indels	0;
			Gaps	0;

DQ

1 ELTQSPSSVSA SVGDRVTITTCASQGSISSLWAWQHQPGRAPKLLIYASSLQSGVPSTRF 60
||| | : ||| | : ||| | : ||| |
2 ELTQSPSSLSA SVGDRTITTCRASQSISSYLWNVQQPKRAPKLIIYAASSLQSGVPSRF 61

```

QY      61 SSGSGYDPSLTISLQFEDATYYCQQANSFPTFGQGTKEIKR 106
      ||||| : ||||| ||||| ||||| : |||||
Db      62 SSGSGDSTLTISLQPEFATYYCQQLNSYPYTFGGQTKLEIKR 107

```

RESULT 14
US-09-848

```

US-09-848-798-40
/ Sequence 40, Application US/09848798
/ Patent No. 6858719
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Donald L.
/ TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
/ TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
/ FILE REFERENCE: 09596-4202
/ CURRENT APPLICATION NUMBER: US/09/848, 798
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 40
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) chain I09
US-09-848-798-40

```

Query Match	84.3%	Score 463;	DB 2;	Length 107;
Best Local Similarity	85.8%;	Pred. No. 2.7e-36;		
Matches	91;	Conservative	7;	Mismatches 8; Indels 0; Gaps 0

```

Qy      1 ELTQSSSVASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVSRF 600
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 ELTQSSSLASVGDRTVITTCRASQGISWLAHYQHPGKAPKLLIYAASSLSQGVSRF 610

```

```
QY      61 SSGSGYCTPSLTITSSLQFEDSATYYCQQANSFPYTFGGTKVEIKR 100
      ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      62 SSGSGGTSTLTITSSLPEDFATYYCQQLNSYPYTFGGTKLEIKR 100
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RESULT 15
ITE-08-376

US-08-276-852-104
: Sequence 104, Application US/08276852
: Patent No. 5652138
: GENERAL INFORMATION:
: APPLICANT: Burton, Dennis R
: APPLICANT: Barbas, Carlos F
: APPLICANT: Lerner, Richard A
: TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
: TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
: NUMBER OF SEQUENCES: 170
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
: STREET: Mail Drop TPC8
: CITY: La Jolla

```

1 STATE: CA
2 COUNTRY: USA
3 ZIP: 92037
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patentn Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/276,852
11 FILING DATE: 18-JUL-1994
12 CLASSIFICATION: 514
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/178,302
15 FILING DATE: 30-SEP-1993
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 07/954,148
18 FILING DATE: 30-SEP-1992
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Fitting, Thomas
21 REGISTRATION NUMBER: 34,163
22 REFERENCE/DOCKET NUMBER: SCR1452P
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 619-554-2937
25 TELEFAX: 619-554-6312
26 INFORMATION FOR SEQ ID NO: 104:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 107 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 MOLECULE TYPE: protein
32 US-08-276-852-104

```

Query Match	83.8%;	Score 460;	DB 1;	Length 107;
Best Local Similarity	85.8%;	Pred. No. 5.1e-36;		
Matches 91;	Conservative 7;	Mismatches 8;	Indels 0;	Gaps 0;

QY	Db	QY	Db
ELTSPSSVASVDRTITICRASQGISWLAHYCHQPGCAPLLTIYSASLSQSGVPSRF	1	ELTSPSSLASVDRTITICRASQGISSTVLMNYQOKPGCAPLLTIYASLSQSGVPSRF	60
61	61	61	61
SGSGGTGDFSLTISLSLOPEDSATYTYCQQAHSFYTTGCGCTKVIKR	106	SGSGSGTDFSLTISLSLOPEDSATYTYCQQAHSFYTTGCGCTKVIKR	106
61	61	61	61
SGSSSGTDFSLTISLSLOPEDSATYTYCQQAHSFYTTGCGCTKVIKR	106	SGSSSGTDFSLTISLSLOPEDSATYTYCQQAHSFYTTGCGCTKVIKR	106

Search completed: August 30, 2006, 00:37:10
job time : 15.4545 secs

Search completed: August 30, 2006, 00:37:10
Job time : 15.4545 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 60.7091 Seconds
(without alignments)
808.788 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGRVTIT.....QQANSFPTFGQGTKEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	4	US-10-027-725A-12
2	499	90.9	107	6	US-11-051-453-4
3	499	90.9	129	6	US-11-051-453-43
4	493	89.8	107	5	US-10-891-658-80
5	491	89.4	107	5	US-10-727-155-312
6	491	89.4	129	5	US-10-910-901-20
7	490	89.3	107	6	US-11-051-453-32
8	490	89.3	129	6	US-11-051-453-36
9	488	89.1	236	5	US-10-910-901-12
10	488	88.9	108	5	US-10-938-353-109
11	487	88.7	107	5	US-10-727-155-122
12	486	88.5	108	5	US-10-938-353-117
13	485	88.3	107	5	US-10-982-359-67
14	484	88.2	123	4	US-10-693-629-66
15	483	88.0	129	5	US-10-910-901-19
16	482	87.8	107	4	US-10-309-762-159
17	482	87.8	155	6	US-11-131-648-14
18	482	87.8	155	6	US-11-131-648-37
19	481	87.6	107	4	US-10-282-088-105
20	481	87.6	129	5	US-10-910-901-17
21	479	87.2	107	4	US-10-309-762-62
22	479	87.2	107	4	US-10-309-762-62
23	478	87.1	107	4	US-10-309-762-61
24	478	87.1	107	4	US-10-309-762-61
25	478	87.1	244	3	US-09-880-748-1881
26	478	87.1	244	4	US-10-293-418-1881
27	478	87.1	244	6	US-11-054-515-1881

28	478	87.1	244	6	US-11-266-444-1881	Sequence 1881, Ap
29	477	86.9	107	5	US-10-638-265-76	Sequence 76, Appl
30	477	86.9	107	5	US-10-893-576-177	Sequence 177, App
31	477	86.9	107	5	US-10-956-008-76	Sequence 76, Appl
32	477	86.9	129	5	US-10-893-576-24	Sequence 24, Appl
33	477	86.9	212	5	US-10-513-725-7	Sequence 7, Appl1
34	475	86.5	236	3	US-09-859-053-30	Sequence 30, Appl
35	475	86.5	236	4	US-10-800-250-30	Sequence 30, Appl
36	475	86.5	236	4	US-10-825-105-30	Sequence 30, Appl
37	474	86.3	107	4	US-10-041-860-43	Sequence 43, Appl
38	474	86.3	107	4	US-10-041-860-218	Sequence 218, App
39	474	86.3	107	4	US-10-665-383-64	Sequence 64, Appl
40	474	86.3	236	5	US-10-910-901-16	Sequence 16, Appl
41	473.5	86.2	106	4	US-10-309-762-84	Sequence 84, Appl
42	472	86.0	107	4	US-10-309-762-60	Sequence 60, Appl
43	472	86.0	107	4	US-10-309-762-63	Sequence 63, Appl
44	471	85.8	236	5	US-10-910-901-4	Sequence 4, Appl1
45	468.5	85.3	108	4	US-10-041-860-357	Sequence 357, App

ALIGNMENTS

```
RESULT 1
US-10-027-725A-12
; Sequence 12, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof.
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-12

Query Match      100.0%; Score 549; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ELTQSPSSVSASVGRVTITTCRASQGISGMLAWYHQPKAPKLLIYSASSLSQGVPSRF 60
      |||
DB      1  ELTQSPSSVSASVGRVTITTCRASQGISGMLAWYHQPKAPKLLIYSASSLSQGVPSRF 60
      |||

QY      61  SSGGYTDFSLTITSSIQFEDSATIYYCOANSFPTFGQGTKEIKR 106
      |||
DB      61  SSGGYTDFSLTITSSIQFEDSATIYYCOANSFPTFGQGTKEIKR 106
      |||

RESULT 2
US-11-051-453-4
; Sequence 4, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
```

FILE REFERENCE: MJI-001
CURRENT APPLICATION NUMBER: US/11/051,453
CURRENT FILING DATE: 2005-02-04
PRIORITY APPLICATION NUMBER: 60/542,357
PRIORITY FILING DATE: 2004-02-06
PRIORITY APPLICATION NUMBER: 60/613,854
PRIORITY FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-453-4

Query Match 90.9%; Score 499; DB 6; Length 107;
Best Local Similarity 91.4%; Pred. No. 3.8e-36;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGGTVEIK 105
Db 63 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGGTVEIK 107

RESULT 3

US-11-051-453-43
Sequence 43, Application US/11051453
Publication No. US20050287150A1
GENERAL INFORMATION:
APPLICANT: AMBROSINO, DONNA
APPLICANT: BABCOCK, GREGORY J.
APPLICANT: BROERING, THERESA
APPLICANT: GRAZIANO, ROBERT
APPLICANT: HERNANDEZ, HECTOR JAVIER
APPLICANT: LOWY, ISRAEL
APPLICANT: MANDELL, ROBERT
APPLICANT: MOHRINE, DEBORAH
APPLICANT: THOMAS, JR., WILLIAM D.
APPLICANT: ZHANG, HUI-FEN
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: MJI-001
CURRENT APPLICATION NUMBER: US/11/051,453
CURRENT FILING DATE: 2005-02-04
PRIORITY APPLICATION NUMBER: 60/542,357
PRIORITY FILING DATE: 2004-02-06
PRIORITY APPLICATION NUMBER: 60/613,854
PRIORITY FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 43
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-453-43

Query Match 90.9%; Score 499; DB 6; Length 129;
Best Local Similarity 91.4%; Pred. No. 4.6e-36;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 25 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGGTVEIK 105
Db 85 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGGTVEIK 129

RESULT 4
US-10-891-658-80
Sequence 80, Application US/10891658
Publication No. US20050074821A1
GENERAL INFORMATION:
APPLICANT: KENNETH, WILD
APPLICANT: TREANOR, JAMES
APPLICANT: HUANG, HAICHUN
APPLICANT: INOUE, HEATHER
APPLICANT: ZHANG, TIE J.
APPLICANT: MARTIN, FRANK
TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
FILE REFERENCE: 02-1240
CURRENT APPLICATION NUMBER: US/10/891,658
CURRENT FILING DATE: 2004-07-15
PRIORITY APPLICATION NUMBER: US 60/487,431
PRIORITY FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn version 3.0
SEQ ID NO 80
LENGTH: 107
TYPE: PRT
ORGANISM: homo sapien
US-10-891-658-80

Query Match 89.8%; Score 493; DB 5; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.3e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGGTVEIK 105
Db 63 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGGGTVEIK 107

RESULT 5

US-10-727-155-312
Sequence 312, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchio
APPLICANT: Raffaella Faggioli
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jiana Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: FACTOR AND USES THEREOF
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIORITY APPLICATION NUMBER: 60/430729
PRIORITY FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-312

Query Match 89.4%; Score 491; DB 5; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.9e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 3 QMTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 62
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105
DB 63 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 107

RESULT 6

US-10-910-901-20
Sequence 20, Application US/10910901
Publication No. US20050054019A1
GENERAL INFORMATION:
APPLICANT: MICHAUD, NEIL R., et al.
TITLE OF INVENTION: ANTIBODIES TO C-MET
FILE REFERENCE: ABX-PF5
CURRENT APPLICATION NUMBER: US/10/910,901
PRIOR FILING DATE: 2004-08-03
PRIOR APPLICATION NUMBER: US 60/492,432
PRIOR FILING DATE: 2003-08-04
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 20
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-10-910-901-20

Query Match 89.4%; Score 491; DB 5; Length 129;
Best Local Similarity 90.5%; Pred. No. 2.3e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 25 QMTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 84
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105
DB 85 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 129

RESULT 7

US-11-051-453-32
Sequence 32, Application US/11051453
Publication No. US20050287150A1
GENERAL INFORMATION:
APPLICANT: AMBROSINO, DONNA
APPLICANT: BABCOCK, GREGORY J.
APPLICANT: BROERING, THERESA
APPLICANT: GRAZIANO, ROBERT
APPLICANT: HERNANDEZ, HECTOR JAVIER
APPLICANT: LOWY, ISRAEL
APPLICANT: MANDELL, ROBERT
APPLICANT: MOLRINE, DEBORAH
APPLICANT: THOMAS, JR., WILLIAM D.
APPLICANT: ZHANG, HUI-PEN
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: MJI-001
CURRENT APPLICATION NUMBER: US/11/051,453
PRIOR FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,357
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 60/613,854
PRIOR FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 32
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-453-32

Query Match 89.3%; Score 490; DB 6; Length 107;
Best Local Similarity 89.5%; Pred. No. 2.3e-35;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 3 QMTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 62
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105
DB 63 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 107

RESULT 8

US-11-051-453-46
Sequence 46, Application US/11051453
Publication No. US20050287150A1
GENERAL INFORMATION:
APPLICANT: AMBROSINO, DONNA
APPLICANT: BABCOCK, GREGORY J.
APPLICANT: BROERING, THERESA
APPLICANT: GRAZIANO, ROBERT
APPLICANT: HERNANDEZ, HECTOR JAVIER
APPLICANT: LOWY, ISRAEL
APPLICANT: MANDELL, ROBERT
APPLICANT: MOLRINE, DEBORAH
APPLICANT: THOMAS, JR., WILLIAM D.
APPLICANT: ZHANG, HUI-PEN
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: MJI-001
CURRENT APPLICATION NUMBER: US/11/051,453
PRIOR FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,357
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 60/613,854
PRIOR FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 46
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-453-46

Query Match 89.3%; Score 490; DB 6; Length 129;
Best Local Similarity 89.5%; Pred. No. 2.8e-35;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 60
DB 25 QMTQSPSSVASVAGDVTITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLOSQVPSRF 84
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105
DB 85 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 129

RESULT 9

US-10-910-901-12
Sequence 12, Application US/10910901
Publication No. US20050054019A1
GENERAL INFORMATION:
APPLICANT: MICHAUD, NEIL R., et al.
TITLE OF INVENTION: ANTIBODIES TO C-MET
FILE REFERENCE: ABX-PF5
CURRENT APPLICATION NUMBER: US/10/910,901

;; CURRENT FILING DATE: 2004-08-03
;; PRIOR APPLICATION NUMBER: US 60/492,432
;; PRIOR FILING DATE: 2003-08-04
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 12
;; LENGTH: 236
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-10-910-901-12

Query Match 89.1%; Score 489; DB 5; Length 236;
Best Local Similarity 89.6%; Pred. No. 6.2e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 25 QMTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQOKPKAPKLLIYAASSLSQGVPSRF 84

QY 61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
Db 85 SSGSGGTDFTLTITSSLOFEDPATYTCQOANSFPTTFGQGTKEIKR 130

RESULT 10
US-10-938-353-109
;; Sequence 109, Application US/10938353
;; Publication No. US20050059113A1
;; GENERAL INFORMATION:
;; APPLICANT: BEDIAN, VAHE
;; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
;; APPLICANT: FOLTZ, IAN
;; APPLICANT: HAAK-FRENDSCHO, MARY
;; APPLICANT: KELLERMANN, SIRID-AIMEE
;; APPLICANT: LOW, JOSEPH EDWIN
;; APPLICANT: MOBLEY, JAMES LESLIE
;; TITLE OF INVENTION: ANTIBODIES TO M-CSF
;; FILE REFERENCE: ABX-PF4
;; CURRENT APPLICATION NUMBER: US/10/938,353
;; CURRENT FILING DATE: 2004-09-09
;; PRIOR APPLICATION NUMBER: 60/502,163
;; PRIOR FILING DATE: 2003-09-10
;; NUMBER OF SEQ ID NOS: 117
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 109
;; LENGTH: 108
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-10-938-353-109

Query Match 88.9%; Score 488; DB 5; Length 108;
Best Local Similarity 88.7%; Pred. No. 3.5e-35;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQOKPKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
Db 63 SSGSGGTDFTLTITSSLOFEDPATYTCQOANSFPTTFGQGTKEIKR 108

RESULT 11
US-10-727-155-122

;; Sequence 122, Application US/10727155
;; Publication No. US20050049402A1
;; GENERAL INFORMATION:
;; APPLICANT: John S. Babcock
;; APPLICANT: Jaspal S. Kang
;; APPLICANT: Orit Foord
;; APPLICANT: Larry Green
;; APPLICANT: Xiao Feng

;; APPLICANT: Scott Kikamp
;; APPLICANT: Mary Haak-Frendescho
;; APPLICANT: Palaniswami Rathanaswami
;; APPLICANT: Craig Pigott
;; APPLICANT: Meina Liang
;; APPLICANT: Rozanne Lee
;; APPLICANT: Kathy Manchulenchio
;; APPLICANT: Rafeaella Faggioli
;; APPLICANT: Giorgio Senaldi
;; APPLICANT: Qiaojuan Jane Su
;; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;; FILE REFERENCE: FACTOR AND USES THEREOF
;; CURRENT APPLICATION NUMBER: US/10/727,155
;; CURRENT FILING DATE: 2003-12-02
;; PRIOR APPLICATION NUMBER: 60/430729
;; PRIOR FILING DATE: 2002-12-02
;; NUMBER OF SEQ ID NOS: 320
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 122
;; LENGTH: 107
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-10-727-155-122

Query Match 88.7%; Score 487; DB 5; Length 107;
Best Local Similarity 89.5%; Pred. No. 4.3e-35;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQOKPKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 105
Db 63 SSGSGGTDFTLTITSSLOFEDFASYTCQOANSFPTTFGQGTKEIKR 107

RESULT 12
US-10-938-353-117
;; Sequence 117, Application US/10938353
;; Publication No. US20050059113A1
;; GENERAL INFORMATION:
;; APPLICANT: BEDIAN, VAHE
;; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
;; APPLICANT: FOLTZ, IAN
;; APPLICANT: HAAK-FRENDSCHO, MARY
;; APPLICANT: KELLERMANN, SIRID-AIMEE
;; APPLICANT: LOW, JOSEPH EDWIN
;; APPLICANT: MOBLEY, JAMES LESLIE
;; TITLE OF INVENTION: ANTIBODIES TO M-CSF
;; FILE REFERENCE: ABX-PF4
;; CURRENT APPLICATION NUMBER: US/10/938,353
;; CURRENT FILING DATE: 2004-09-09
;; PRIOR APPLICATION NUMBER: 60/502,163
;; PRIOR FILING DATE: 2003-09-10
;; NUMBER OF SEQ ID NOS: 117
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 117
;; LENGTH: 108
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-10-938-353-117

Query Match 88.5%; Score 486; DB 5; Length 108;
Best Local Similarity 89.6%; Pred. No. 5.3e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSAASVGDRTVITTCRASQGISWLAHYQOKPKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106

Db 63 SSGSGTDFLTITSSLPEDFATYYCOQANSFPLTGGTKVEIKR 108

RESULT 13

US-10-982-359-67
 ; Sequence 67, Application US/10982359
 ; Publication No. US20050112694A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, Paul J.
 ; APPLICANT: Zhou, Hongxing
 ; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
 ; FILE REFERENCE: 3492-A
 ; CURRENT APPLICATION NUMBER: US/10/982,359
 ; PRIOR FILING DATE: 2004-11-04
 ; PRIOR APPLICATION NUMBER: 60/518,166
 ; PRIOR FILING DATE: 2003-11-07
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 67
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: 63 light chain variable region
 US-10-982-359-67

Query Match 88.3%; Score 485; DB 5; Length 107;
 Best Local Similarity 88.6%; Pred. No. 6,4e-35;
 Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 3 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 62
 Qy 61 SSGSGTDFSLTITSSLPEDSATYYCOQANSFPYTGQTKVEIK 105
 Db 63 SSGSGTDFLTITSSLPEDFATYYCOQANSFPFTGPGTKVDIK 107

RESULT 14

US-10-693-629-66
 ; Sequence 66, Application US/10693629
 ; Publication No. US20040120948A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 ; APPLICANT: MIKAYAMA, Toshitumi
 ; APPLICANT: YOSHIDA, Hitoshi
 ; APPLICANT: FORCE, Walker, R.
 ; APPLICANT: CHEN, Kingjie
 ; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
 ; FILE REFERENCE: 021286-0306473
 ; CURRENT APPLICATION NUMBER: US/10/693,629
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: PCT/US01/13672
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US09/844,684
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: JP2001/142482
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: JP2001/310535
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: US10/040,244
 ; PRIOR FILING DATE: 2001-10-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 66
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-693-629-66

Query Match 88.2%; Score 484; DB 4; Length 223;
 Best Local Similarity 87.7%; Pred. No. 1.6e-34;
 Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 25 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYASSLSQGVPSRF 84
 Qy 61 SSGSGTDFSLTITSSLPEDSATYYCOQANSFPYTGQTKVEIKR 106
 Db 85 SSGSGTDFLTITSSLPEDFATYYCOQANSFPFTGPGTKVDIKR 130

RESULT 15

US-10-910-901-19
 ; Sequence 19, Application US/10910901
 ; Publication No. US20050054019A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MICHAUD, NEIL R., et al.
 ; TITLE OF INVENTION: ANTIBODIES TO c-MET
 ; FILE REFERENCE: ABX-PF5
 ; CURRENT APPLICATION NUMBER: US/10/910,901
 ; CURRENT FILING DATE: 2004-08-03
 ; PRIOR APPLICATION NUMBER: US 60/492,432
 ; PRIOR FILING DATE: 2003-08-04
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 19
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-910-901-19

Query Match 88.0%; Score 483; DB 5; Length 129;
 Best Local Similarity 88.6%; Pred. No. 1.2e-34;
 Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
 Db 25 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYASSLSQGVPSRF 84
 Qy 61 SSGSGTDFSLTITSSLPEDSATYYCOQANSFPYTGQTKVEIK 105
 Db 85 SSGSGTDFLTITSSLPEDFATYYCOQANSFPFTGPGTKVDIK 129

Search completed: August 30, 2006, 00:50:39
 Job time : 60.7091 secs

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OM protein - :protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 12.5273 Seconds
(without alignments)
578.960 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGDVVTIT.....QQANSPFTFGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications_AA_New:*

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- 3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 8: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	88.9	108	7	US-11-375-221-109 Sequence 109, App
2	486	88.5	108	7	US-11-375-221-117 Sequence 117, App
3	484	88.2	108	6	US-10-981-300-27 Sequence 27, App1
4	484	88.2	155	6	US-10-981-300-2 Sequence 2, App1
5	482	87.8	234	6	US-10-511-436A-92 Sequence 92, App1
6	481	87.6	107	7	US-11-211-917-105 Sequence 105, App1
7	476	86.7	106	6	US-10-981-300-26 Sequence 26, App1
8	468	85.2	234	7	US-11-211-917-24 Sequence 24, App1
9	465	84.9	234	7	US-11-211-917-48 Sequence 48, App1
10	463	84.3	107	7	US-11-211-917-20 Sequence 20, App1
11	463	84.3	107	7	US-11-328-483-40 Sequence 40, App1
12	461	84.0	107	7	US-11-211-917-44 Sequence 44, App1
13	460	83.8	108	7	US-11-254-182-27 Sequence 27, App1
14	460	83.8	108	7	US-11-219-121-23 Sequence 23, App1
15	460	83.8	108	7	US-11-106-762-19 Sequence 19, App1
16	460	83.8	108	7	US-11-238-281-3 Sequence 3, App1
17	460	83.8	108	7	US-11-136-917A-11 Sequence 11, App1
18	460	83.8	214	7	US-11-219-121-27 Sequence 27, App1
19	459	83.6	236	7	US-11-375-221-20 Sequence 20, App1
20	457	83.2	107	7	US-11-328-483-175 Sequence 175, App
21	457	83.2	107	7	US-11-328-483-176 Sequence 176, App
22	457	83.2	291	7	US-11-154-103-10 Sequence 10, App1
23	456	83.1	107	7	US-11-328-483-156 Sequence 156, App
24	456	83.1	108	6	US-10-981-300-21 Sequence 21, App1
25	455	82.9	107	7	US-11-254-182-5 Sequence 5, App1

26	455	82.9	107	7	US-11-295-229-5 Sequence 5, App1
27	455	82.9	107	7	US-11-154-091-5 Sequence 5, App1
28	455	82.9	108	7	US-11-370-301-21 Sequence 21, App1
29	455	82.9	108	7	US-11-370-301-21 Sequence 21, App1
30	454	82.7	107	7	US-11-145-131A-26 Sequence 26, App1
31	454	82.7	109	7	US-11-504-986-14 Sequence 14, App1
32	453	82.5	106	7	US-11-337-300-41 Sequence 41, App1
33	453	82.5	243	7	US-11-337-300-47 Sequence 47, App1
34	453	82.5	244	7	US-11-317-786B-17 Sequence 17, App1
35	453	82.5	244	7	US-11-317-786B-19 Sequence 19, App1
36	453	82.5	245	7	US-11-337-300-51 Sequence 51, App1
37	453	82.5	245	7	US-11-337-300-53 Sequence 53, App1
38	453	82.5	245	7	US-11-337-300-59 Sequence 59, App1
39	453	82.5	245	7	US-11-337-300-63 Sequence 63, App1
40	453	82.5	247	7	US-11-337-300-57 Sequence 57, App1
41	453	82.5	247	7	US-11-337-300-96 Sequence 96, App1
42	453	82.5	248	7	US-11-337-300-61 Sequence 61, App1
43	453	82.5	249	7	US-11-337-300-49 Sequence 49, App1
44	453	82.5	249	7	US-11-337-300-67 Sequence 67, App1
45	453	82.5	249	7	US-11-337-300-69 Sequence 69, App1

ALIGNMENTS

```
RESULT 1
US-11-375-221-109
; Sequence 109, Application US/11375221
; Publication No. US20060153850A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENSCH, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PP4
; CURRENT APPLICATION NUMBER: US/11/375,221
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US/10/938,353
; PRIOR FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patent Ver. 3.2
; SEQ ID NO 109
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-375-221-109

Query Match      88.9%; Score 488; DB 7; Length 108;
Best Local Similarity 88.7%; Pred. No. 4.4e-38;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYOHQPGKAPKLLYSASLSQSVSRF 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      3 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQKPGKAPKLLIYASLSQSVSRF 62
QY      61 SSGSGYGFDSLTITSSLOPEDSATYTYCOQANSFPTFGQGTKEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      63 SSGSGGTDFTLTITSSLOPEDFATYTYCOQANSFPTFGQGTKEIKR 108

RESULT 2
US-11-375-221-117
; Sequence 117, Application US/11375221
; Publication No. US20060153850A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
```

```

? APPLICANT: FOLTZ, IAN
? APPLICANT: HAAK-FRENSCH, MARY
? APPLICANT: KELLERMAN, SIRID-AIMEE
? APPLICANT: LOW, JOSEPH EDWIN
? APPLICANT: MOHLEY, JAMES LESLIE
? TITLE OR INVENTION: ANTIBODIES TO M-CSF
? FILE REFERENCE: ABX-PP4
? CURRENT APPLICATION NUMBER: US/11/375, 221
? CURRENT FILING DATE: 2006-03-13
? PRIOR APPLICATION NUMBER: US/10/938, 353
? PRIOR FILING DATE: 2004-09-09
? PRIOR APPLICATION NUMBER: 60/502, 163
? PRIOR FILING DATE: 2003-09-10
? NUMBER OF SEQ ID NOS: 117
? SOFTWARE: PatentIn Ver. 3.2
? SEQ ID NO 117
? LENGTH: 108
? TYPE: PRF
? ORGANISM: Homo sapiens
? US-11-375-221-117

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Query Match	88.5%;	Score 486;	DB 7;	Length 108;
Best Local Similarity	89.6%;	Pred. No. 6.7e-38;		
Matches	95;	Conservative	5;	Mismatches 6;
			Indels	0;
			Gaps	0;

[illegible]

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RESULT 3
US-10-981-300-27
? Sequence 27, Application US/10981300
? Publication No. US20060093599A1
? GENERAL INFORMATION:
? APPLICANT: GIORGIO SENALDI
? APPLICANT: GADI GAZIT-BORNSTEIN
? TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
? TITLE OF INVENTION: FOR MAKING AND USING THE SAME
? FILE REFERENCE: ABGX-005
? CURRENT APPLICATION NUMBER: US/10/981,300
? CURRENT FILING DATE: 2004-11-03
? NUMBER OF SEQ ID NOS: 71
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 108
? TYPE: PRT
? ORGANISM: homo sapiens
US-10-981-300-27

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Query Match	88.2%	Score 484;	DB 6;	Length 108;
Best Local Similarity	89.6%	Pred. No. 1e-37;		
Matches	95;	Conservative	5;	Mismatches 6;
			Indels	0;
			Gaps	0;

Qy	Db	Qy	Db
ELTQSPSPSVASVSDDRVTITFCRAQGGISSMLAWOHQPGAKPKLLIYSASLSQGVSPRF	3	SGSGGYGIDFSLTITSLQPEDSATYYCOANSPFTFPGQGTVEKFR	61
QMTQSPSPSVASVSDDRVTITFCRAQGGISSMLAWQQRKPKAKPKLLIYVASLSQGVSPRF	63	SGSSSGDFTLTITSLQPEDIAIYYCOADSEFTFPGQGTVEKFR	108

RESULT 4
US-10-981-300-2
; Sequence 2, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI

```

? APPLICANT: GADI GAZIT-BORNSTEIN
? TITLE OF INVENTION: ANTI-PROGERIN ANTIBODIES, AND METHODS
? TITLE OF INVENTION: FOR MAKING AND USING THE SAME
? FILE REFERENCE: ABG-005
? CURRENT APPLICATION NUMBER: US/10/981.300
? CURRENT FILING DATE: 2004-11-03
? NUMBER OF SEQ ID NOS: 71
? SOFTWARE: PaeleSO for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 155
? TYPE: PR1
? ORGANISM: homo sapien
? US-10-981-300-2

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Query Match	88.2%;	Score 484;	DB 6;	Length 155;
Best Local Similarity	89.6%;	Pred. No. 1.5e-37;		
Matches 95;	Conservative 5;	Mismatches 6;	Indels 0;	Gaps 0;

Qy	1	ELTQSSSSSVASVAGDVTITTCRASQGISSMILAMYCHQPKADKRLLYVASISLQSGVPSRF	60
	:	:	:
Db	3	QMTPSSSVASVGVDRVTITTCRASQGISSMILAMVYQPKAPKRLLYVASISLQSGVPSRF	62
Qy	61	SGSGGYGDPFSLTSLTLOFEASATYYVCOQANSPFYTGQGTKEIKR	106
	:	:	:
Db	63	SGSGSGTDFTLTSLTLOPEDIATYYCOQADSPFTTGQGTKEIKR	108

```

RESULT 5
US-10-511-436A-92
; Sequence 92, Application US/10511436A
; Publication No. US20060148039A1
GENERAL INFORMATION:
APPLICANT: KOBAYASHI, KAZUO
APPLICANT: KITAGAWA, YOSHINOBU
APPLICANT: KOMEDA, TOSHIOHRO
APPLICANT: KAWASHIMA, NAGAKO
APPLICANT: JIGAMI, YOSHIFUMI
APPLICANT: CHIBA, YASUNORI
TITLE OF INVENTION: METHYLOTROPH PRODUCING MAMMALIAN TYPE SUGAR CHAIN
FILE REFERENCE: 081356-0224
CURRENT APPLICATION NUMBER: US/10/511,436A
CURRENT FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: PCT/JP03/05464
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: JP 2002-127677
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 92
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-436A-92

```

Query March	87.8%;	Score 482;	DB 6;	Length 234;
Best Local Similarity	89.6%;	Pred. No. 3.4e-37;		
Matches 95;	Conservative 5;	Mismatches 6;	Indels 0;	Gaps 0

[illegible]

US-11-211-917-105
; Sequence 105, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE

```
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-105

Query Match      87.6%; Score 481; DB 7; Length 107;
Best Local Similarity 89.5%; Pred. No. 1.9e-37;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPGKAPKLLIYSASSLSQGVPSRF 60
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Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPGKAPKLLIYAASSLQGVPSRF 62
QY 61 SSGSGYGTDFSLTITSSLOFEDSATYYCOQANSFPYTFGGGTKEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGTDFLTITSSLOPEDFATYYCOQANSFPLTFGGGTKEIKR 107
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RESULT 7
US-10-981-300-26
; Sequence 26; Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 106
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-981-300-26
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Query Match      86.7%; Score 476; DB 6; Length 106;
Best Local Similarity 89.6%; Pred. No. 5.5e-37;
Matches 95; Conservative 5; Mismatches 4; Indels 2; Gaps 1;
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QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPGKAPKLLIYAASSLQGVPSRF 62
```

```
QY 61 SSGSGYGTDFSLTITSSLOFEDSATYYCOQANSFPYTFGGGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGTDFLTITSSLOPEDFATYYCOQANSF--TFGGGTKEIKR 106

RESULT 8
US-11-211-917-24
; Sequence 24; Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
```

```
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-24

Query Match      85.2%; Score 468; DB 7; Length 234;
Best Local Similarity 86.8%; Pred. No. 6.6e-36;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
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   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPGKAPKLLIYSASSLSQGVPSRF 82
QY 61 SSGSGYGTDFSLTITSSLOFEDSATYYCOQANSFPYTFGGGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTDFLTITSSLOPEDFATYYCOQANSFPLTFGGGTKEIKR 128
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RESULT 9
US-11-211-917-48
; Sequence 48; Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-48
```

```
Query Match      84.9%; Score 466; DB 7; Length 234;
Best Local Similarity 85.8%; Pred. No. 1e-35;
Matches 91; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYQOKPGKAPKLLIYAASSLQGVPSRF 82
```

```
QY 61 SSGSGYGTDFSLTITSSLOFEDSATYYCOQANSFPYTFGGGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTDFLTITSSLOPEDFATYYCOQANSFPLTFGGGTKEIKR 128

RESULT 10
US-11-211-917-20
```

```
; Sequence 20, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-20
```

```
Query Match      84.3%; Score 463; DB 7; Length 107;
Best Local Similarity 86.7%; Pred. No. 8,6e-36;
Matches 91; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy      1 ELTQSPSSVASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db      3 QMTQSPSSVASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 62
```

```
Qy      61 SSGSGTDFSLTISLQFEDSATYYCOQANSPFTFGGTVKEIK 105
Db      63 SSGSGTDFSLTISLQFEDPATYYCOQTFSPFLFGGTVKEIK 107
```

```
RESULT 11
US-11-328-483-40
; Sequence 40, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 109
US-11-328-483-40
```

```
Query Match      84.3%; Score 463; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 8,6e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 ELTQSPSSVASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db      2 ELTQSPSSIASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYASSLSQGVPSRF 61
```

```
Qy      61 SSGSGTDFSLTISLQFEDSATYYCOQANSPFTFGGTVKEIK 106
Db      62 SSGSGTDFSLTISLQFEDPATYYCOQANSPFTFGGTVKEIK 107
```

```
RESULT 12
US-11-211-917-44
; Sequence 44, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-44
```

```
Query Match      84.0%; Score 461; DB 7; Length 107;
Best Local Similarity 85.7%; Pred. No. 1,3e-35;
Matches 90; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy      1 ELTQSPSSVASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db      3 QMTQSPSSVASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYASTLSQGVPSRF 62
```

```
Qy      61 SSGSGTDFSLTISLQFEDSATYYCOQANSPFTFGGTVKEIK 105
Db      63 SSGSGTDFSLTISLQFEDPATYYCOQANSPFTFGGTVKEIK 107
```

```
RESULT 13
US-11-254-182-27
; Sequence 27, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 27
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-254-182-27
```

```
Query Match      83.8%; Score 460; DB 7; Length 108;
Best Local Similarity 84.0%; Pred. No. 1,6e-35;
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
```

Qy	Db	Qy	Db
1	3	61	63
ELTOSPSSSVASVGRVITITCRASGIGISMTLAWOHQKGA	QMTQSPSSLASVGRVITITCRASGISINYLAWYQKXGKA	SGSGVGDPSLITISLOFEDSATYYCOQANSPRYFGQGTVEI	SGSGSGIDFILITISLOPEDEPATIYYCOQYNLSLPMFFGGIK
VRPFR	PKLITVAASTJESGVPSRF	VRPFR	VEIKR
60	62	106	108

```

Oy      61  SSSGGTDFSLTISLQFEDSATYVCOOANSPFYFGQTKVEIKR 106
Db      63  SSGSGTDFTLTISLQFEDFATYVCOOANSLPWFQGTKEIKR 108

```

Search completed: August 30, 2006, 00:52:03
Job time : 13.5273 secs

```

RESULT 14
US-11-219-121-23
: Sequence 23, Application US/11219121
: Publication No. US20060093601A1
GENERAL INFORMATION:
: APPLICANT: Fong, Sherman
: APPLICANT: Dennis Mark S.
: TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR
: FILE REFERENCE: P21591
: CURRENT APPLICATION NUMBER: US/11/219,121
: CURRENT FILING DATE: 2005-09-02
: PRIOR APPLICATION NUMBER: US 60/607,377
: PRIOR FILING DATE: 2004-09-03
: NUMBER OF SEQ ID NOS: 68
: SEQ ID NO 23
: LENGTH: 108
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: sequence is synthesized
US-11-219-121-23

```

Query Match	83.8%	Score 460;	DB 7;	Length 108;
Best Local Similarity	84.0%	Pred. No. 1.6e-35;		
Matches 89;	Conservative 10;	Mismatches 7;	Indels 0;	Gaps 0;

```
QY 1 ELTQSSSVASVGDRTVITTCRASQGISSTLAWQHQPCKAPKLLIYSASSLSQGPSRF 600
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSSSLASVGDRTVITTCRASQGISSTLAWQHQPCKAPKLLIYAASLSLSEGPSRF 622
```

```
QY      61 SSGSGYGFDSLTISSLQFEDSATYYCQQANSFPTTGGQTKVEIKR 106
      |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      63 SSGSGGDFTLTISSLQPEDFATYYCQQYNLSLPTWTGGQTKVEIKR 108
```

```

1 RESULT 15
2 US-11-106-762-19
3 : Sequence 19, Application US/11/06762
4 : Publication No. US20060093662A1
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: CHINTHARAPATI, ANAN ET AL.
9 :
10 : TITLE OF INVENTION: ASSAY FOR ANTIBODIES
11 :
12 : FILE REFERENCE: P2075R1
13 :
14 : CURRENT APPLICATION NUMBER: US/11/106,762
15 :
16 : CURRENT FILING DATE: 2005-04-15
17 :
18 : PRIOR APPLICATION NUMBER: US 60/563,193
19 :
20 : PRIOR FILING DATE: 2004-04-16
21 :
22 : NUMBER OF SEQ ID NOS: 39
23 :
24 : SEQ ID NO 19
25 :
26 : LENGTH: 108
27 :
28 : TYPE: prt
29 :
30 : ORGANISM: Artificial sequence
31 :
32 : FEATURE:
33 :
34 : OTHER INFORMATION: Sequence is synthesized
35 :
36 : US-11-106-762-19

```

Query Match	83.8%	Score 460	DB 7	Length 108
Best Local Similarity	84.0%	Pred. No. 1.6e-35		
Matches 89, Conservative	10	Mismatches 7	Indels 0	Gaps 0

```

Qy      1  ELTQSPSSVSASVGDRTVITTCRASQGISLWLTQHQPGRAPKLLYSASSLQSGVPSRF 600
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      3  QMTQSPSSLSASVGDRTVITTCRASQGISLWLTQHQPGRAPKLLIYAASSLSGVPSPRF 620

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